

095Y35
ID 095Y35 PRELIMINARY; PRT; 327 AA.
AC 095Y35;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHEICAL 38.2 KDA PROTEIN.
GN Y108G3AL.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdita; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT Investigating biology. The C. elegans Sequencing Consortium. "
RT Science 283:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Courtney L.;
RT "The sequence of C. elegans cosmid Y108G3AL.";
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission".
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: ACO24744; AAK72068.1; -.
KW Hypothetical protein.
SQ SEQUENCE 327 AA; 38186 MW; ASE291465E1BCF67 CRC64;

Query Match 84.8%; Score 28; DB 5; Length 327;
Best Local Similarity 85.7%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 144 FNLKISR 150
RESULT 14
ID 09CUT6 PRELIMINARY; PRT; 346 AA.
AC 09CUT6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE 1110021E09RIK PROTEIN (FRAGMENT).
GN 1110021E09RIK.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hornum M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
RA Wyszewski H., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK015938; BAB30042.1; -.
DR MGI: 1914171; 1110021E09RIK.
FT NON_TER 346 346
SQ SEQUENCE 346 AA; 39909 MW; FFCBCEFF7A90DE95 CRC64;

Query Match 84.8%; Score 28; DB 11; Length 346;
Best Local Similarity 71.4%; Pred. No. 88;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 137 FTLKISR 143
RESULT 15
ID 093XF8 PRELIMINARY; PRT; 347 AA.
AC 093XF8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE KINESIN HEAVY CHAIN (FRAGMENT).
GN KIN6.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-WHOLE KERNELS;
RA Lawrence C.J., Mainberg R.L., Muszynski M.G., Dawe R.K.;
RT "Maximum likelihood methods reveal conservation of function among
RT closely related kinesin families.";
RL J. Mol. Evol. 0:0-0(2001).
DR EMBL: AF272754; AAK91817.1; -.
FT NON_TER 1 1
SQ SEQUENCE 347 AA; 37914 MW; 889AEF07B56F62BA CRC64;

QY 1 FTLKIS 6
Db 221 FTLKIS 226
Query Match 84.8%; Score 28; DB 10; Length 347;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: July 15, 2002, 13:22:46
Job time: 1482 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 12:57:57 ; Search time 228.39 Seconds
(without alignments)
3.404 Million cell updates/sec

Title: US-09-712-819A-6
Sequence: 1 FTAKISR 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.GeneSeq.032802:*
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2: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*
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15: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:*
16: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*
17: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:*
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20: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	32	19	AAW79207
2	33	100.0	32	22	AAAB6295
3	33	100.0	81	17	AAAR2994
4	33	100.0	89	16	AAAR0082
5	33	100.0	92	13	AAAR27009
6	33	100.0	93	21	AAV56570
7	33	100.0	100	16	AAAR72067
8	33	100.0	100	16	AAAR72066
9	33	100.0	100	22	AAE12711
10	33	100.0	100	22	AAE06958
11	33	100.0	100	22	AAE06959

12	33	100.0	100	22	AAE06960	Mouse germline kap
13	33	100.0	100	22	AAE06961	Mouse germline kap
14	33	100.0	100	22	AAE06962	Mouse germline kap
15	33	100.0	100	22	AAE06963	Mouse germline kap
16	33	100.0	100	22	AAE06964	Mouse germline kap
17	33	100.0	100	22	AAE06965	Mouse germline kap
18	33	100.0	100	22	AAE06966	Mouse germline kap
19	33	100.0	100	22	AAE06967	Mouse germline kap
20	33	100.0	101	14	AAAR6529	Light chain variab
21	33	100.0	104	18	AAAR6529	Anti-DNA antibody
22	33	100.0	106	22	ABBA3489	Peptide #10995 enc
23	33	100.0	106	22	ABB26451	Protein #8450 enc
24	33	100.0	106	22	AAAB4423	Human brain expres
25	33	100.0	106	22	AAAR7235	Human bone marrow
26	33	100.0	106	22	AAAR21171	Peptide #7605 enco
27	33	100.0	106	22	AAAR37382	Peptide #11419 enc
28	33	100.0	108	14	AAAR38594	Human lambda light
29	33	100.0	108	19	AAAR58494	Human kappa light
30	33	100.0	109	20	AAAR39809	TR1.6 antibody lig
31	33	100.0	110	14	AAAR38159	Sequence of the 11
32	33	100.0	110	22	AAAR77580	Human bone marrow
33	33	100.0	111	13	AAAR42808	RSV19 Vx. Mus mus
34	33	100.0	111	14	AAAR42803	RSV19 Vx. Mus mus
35	33	100.0	111	17	AAAR9849	Murine antibody 58
36	33	100.0	111	21	AAAR95225	Anti-platelet glyc
37	33	100.0	111	21	AAAR95227	Human HF-21/28 kap
38	33	100.0	111	22	AAE06948	Human kappa light
39	33	100.0	111	22	AAE06948	Human kappa light
40	33	100.0	112	14	AAAR32239	Humanised Mab ligh
41	33	100.0	112	15	AAAR32058	Light chain variab
42	33	100.0	112	16	AAAR82961	Antibody 3S193 lig
43	33	100.0	112	16	AAAR68741	Mab B3 light chain
44	33	100.0	112	16	AAAR79248	Light chain variab
45	33	100.0	112	17	AAAR95217	B3 immunoglobulin

ALIGNMENTS

RESULT	ID	AAW79207	standard; Protein; 32 AA.
XX	XX	AAW79207	
AC	AC	AAW79207	
XX	XX	21-DEC-1998 (first entry)	
DE	DE	Framework 3 region of human V kappa gene HUM5400.	
XX	XX		
KM	KM	Monoclonal antibody; Mab; LO-CD2a; humanised antibody; CD2 antigen;	
KW	KW	human lymphocyte; immune response; chimeric; graft-versus-host disease;	
XX	XX	T-cell; transplant rejection; autoimmune disease; HUM5400.	
OS	OS	Homo sapiens.	
XX	XX		
PN	PN	US5817311-A.	
XX	XX		
PD	PD	06-OCT-1998.	
XX	XX		
PF	PF	07-JUN-1995; 95US-0472281.	
XX	XX		
PR	PR	07-JUN-1995; 95US-0472281.	
PR	PR	05-MAR-1993; 93US-0027008.	
PR	PR	09-SEP-1993; 93US-0119032.	
XX	XX	29-MAR-1995; 95US-0407009.	
PA	PA	(UYLO-) UNIV CATHOLIQUE LOUVAIN.	
PI	PI		
XX	XX	Bazin H, Latime D;	
XX	XX		
DR	DR	WPI; 1998-556337/47.	
XX	XX		
PT	PT	Inhibition of T-cell mediated immune response with anti-CD2	

PT monoclonal antibody IO-CD2a - used for preventing transplant
PT rejection or for treating graft-versus-host disease or auto-immune
PT diseases
PS Example 7; Columns 33-34; 96pp; English.
XX
XX
CC This represents the amino acid sequence of the framework 3 region of
CC human V kappa gene HUM5400. This is used to construct a humanised antibody
CC LO-CD2a. The invention relates to the use of the monoclonal antibody
CC (Mab) LO-CD2a or a humanised or a chimeric version of the LO-CD2a
CC antibody for the inhibition of a T-cell mediated immune response in a
CC patient. The Mab LO-CD2a (produced by hybridoma cell line ATCC HB 11423)
CC can bind to an epitope on the CD2 antigen of the human lymphocytes. The
CC T-cell mediated immune response in a patient can be inhibited by
CC administering the Mab LO-CD2a or an antibody that binds to the same
CC human lymphocyte epitope as LO-CD2a. The method is used for preventing
CC transplant rejection or for treating graft-versus-host disease or for
CC treating autoimmune diseases.
SQ Sequence 32 AA;

Query Match 100.0%; Score 33; DB 19; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
Db 15 ftklstr 21
| | | | |
| | | | |

RESULT 2
AAB86295 standard; peptide: 32 AA.
XX
XX AAB86295;
XX
XX 13-SEP-2001 (first entry)
XX
DE Murine derived antibody Wue-1 light chain variable region FW-3.
XX
XX Antibody; Wue-1; variable region; light chain; heavy chain; antitumor;
KW Immunomodulatory; cognate antigen identification; autoimmune disease;
KW tumor; multiple myeloma; lymphoma; plasmacytoma; FW-3.
XX
XX Mus sp.
XX
XX OS
XX PN DE19962583-A1.
XX
XX PD 28-JUN-2001.
XX
XX PF 23-DEC-1999; 99DE-1062583.
XX
XX PR 23-DEC-1999; 99DE-1062583.
XX
XX PA (MUEL/) MUELLER-HERMELINK H K.
XX (GREI/) GREINER A.
XX
XX PI Mueller-Hermelink HK, Greiner A;
XX
XX DR WPI; 2001-426596/46.
XX
XX PT New antibodies specific for plasma cells, useful for treatment and
XX diagnosis of autoimmune diseases and plasma cell tumors -
XX
XX PS Claim 1; Page 10; 18pp; German.
XX
CC This invention describes novel antibodies (Ab) in which the variable
CC region (VR) of at least one chain and/or the VR of at least one heavy
CC chain includes at least one of 7 specified sequences, or fragments of
CC these sequences, or contain at least one light chain and/or heavy
CC chain encoded by specific nucleic acid sequences (I) and (II),
CC reproduced, or their fragments. The products of the invention have

CC antitumor and immunomodulatory activity. Ab, or other antibodies that
CC recognize the same antigen, are used: (i) to identify cognate antigens;
CC (ii) for specific labeling of plasma cells (PC), for identification or
CC separation, e.g. in an extracorporeal system; (iii) for generating
CC additional antibodies able to label PC; and (iv) for treating autoimmune
CC diseases and/or tumors, e.g. multiple myeloma, lymphoma and/or
CC plasmacytoma. Ab are specific for mature PC, i.e. they do not recognize
CC precursor stages, even though these precursors are used as immunogens. As
CC therapeutic agents, they should show fewer side effects than conventional
CC chemotherapeutic agents. This sequence represents the Wue-1 antibody
CC variable region light chain FW-3 fragment described in the method of the
CC invention.
SQ Sequence 32 AA;

Query Match 100.0%; Score 33; DB 22; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
Db 15 ftklstr 21
| | | | |
| | | | |

RESULT 3
AAR92994 standard; Protein: 81 AA.
XX
XX AAR92994;
XX
XX 18-MAY-1996 (first entry)
XX
DE Homologous sequences to antibody IOR-R3 variable region light chain.
XX
XX
XX IOR-R3; monoclonal antibody; human; mouse; light chain; homology;
KW variable region; epidermal growth factor receptor; hybridoma;
KW framework; cloning; computer; algorithm; immunogenicity;
KW site-directed mutagenesis; T-lymphocyte epitope; tertiary structure;
KW point mutation; antibody engineering; protein engineering;
KW humanised antibody; antitumour; cancer; therapy.
XX
XX OS
XX FH Homo sapiens.
XX
XX FH
XX Key
XX Location/Qualifiers
XX 2
XX /note= "Amino acid involved in tertiary structure"
XX 4
XX /note= "Amino acid involved in tertiary structure"
XX 24..25
XX /note= "Amino acids involved in tertiary structure"
XX 35..39
XX /note= "Amino acids involved in tertiary structure"
XX 46
XX /note= "Amino acid involved in tertiary structure"
XX 48
XX /note= "Amino acid involved in tertiary structure"
XX 50..51
XX /note= "Amino acids involved in tertiary structure"
XX 53
XX /note= "Amino acid involved in tertiary structure"
XX 71
XX /note= "Amino acid involved in tertiary structure"
XX
XX EP699755-A2.
XX
XX PN 06-MAR-1996.
XX
XX PD 27-JUN-1995; 95EP-0201752.
XX
XX PF 30-JUN-1994; 94CU-0000080.
XX
XX PR (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
XX
XX PA

XX Mateo de Acosta del Rio CM, Rodriguez RP, Valladares JL;
XX WPI: 1996-130770/14.
XX
XX Identifying interspecies differences in amino acid sequence of Ig
PT T-cell epitopes - by sequence comparison, also humanised antibodies
PT contg. altered T-cell epitopes, retaining antigen specificity but
PT not immunogenicity, esp. for tumour treatment
XX
PS Claim 14; Fig 3; 33pp: English.
XX
XX The sequence represents residues from a human immunoglobulin with
CC homology to the light chain variable region from monoclonal antibody
CC IOR-R3 (AAR92993), specific for epidermal growth factor receptor,
CC produced by a mouse hybridoma. The sequence is partial, and
CC complementarily determining regions are omitted. The sequence is
CC isolated by comparison of human and mouse immunoglobulins and
CC analysis for T-lymphocyte antigenic sequences using a computer
CC algorithm. Residues not within a complementarity determining region,
CC canonical structure or Verrier zone may be modified to reduce
CC immunogenicity in humans (e.g. in sequence AAR92993). This method,
CC which involves the introduction of only a few point mutations into
CC T-cell epitope coding regions, is generally applicable in humanisation
CC of mouse antibodies. The resulting humanised antibodies may be used
CC e.g. as antitumour agents. They retain the antigen recognition of the
CC original antibody, but are not immunogenic in humans.
XX
SQ Sequence 81 AA:

Query Match 100.0%; Score 33; DB 17; Length 81;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 53 ftklkr 59

RESULT 4
AAR80082
ID AAR80082 standard; Protein; 89 AA.
XX
XX AAR80082;
AC
XX
XX 22-MAY-1996 (first entry)
DT
XX
XX Mouse derived light chain RT3 phage antibody pattern I.
DE
XX
XX Light chain; RT3; murine; catalytic antibody; bacteriophage;
KW pattern I.
XX
XX Mus musculus.
OS
XX
XX Key
FH Location/Qualifiers
FT 1..14
FT Region /note= "Framework region 1"
FT 15..28
FT Region /note= "complementarity determining region 1"
FT 29..42
FT Region /note= "Framework region 2"
FT 43..49
FT Region /note= "complementarity determining region 2"
FT 50..82
FT Region /note= "Framework region 3"
FT 83..89
FT Region /note= "complementarity determining region 3
N-terminal fragment"
XX
XX W09527045-A1.
XX 12-Oct-1995.
PD

XX 30-MAR-1994; 94MO-US03420.
PF
XX 30-MAR-1994; 94MO-US03420.
PR
XX (IGEN-) IGEN INC.
XX
XX Chiswell D, Darsley MJ, Fitzgerald K, Keenan JH;
PI Martin MR, Mc Cafferty J, Smith RG, Tittus RC, Williams RO;
PI WPI: 1995-358624/46.
DR
XX N-PSDB: AAT04629.
XX
XX Production of catalytic antibodies displayed on phage - by
PT generating a gene library of antibody-derived domains and expressing
PT it in phage vectors
XX
XX Disclosure; Fig 10; 133pp: English.
PS
XX AAT04629 encodes AAR80082 mouse derived light chain RT3 phage antibody.
CC The DNA was used in the prepn. of catalytic antibody (CA) producing
CC bacteriophage. The CAs can be used to activate/deactivate a
CC biological function in an animal by enhancing the rate of cleavage,
CC or formation of a specific bond within a mol. in vivo.
XX
SQ Sequence 89 AA:

Query Match 100.0%; Score 33; DB 16; Length 89;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTLKISR 7
Db 65 ftklkr 71

RESULT 5
AAR27009
ID AAR27009 standard; peptide; 92 AA.
XX
XX AAR27009;
AC
XX
XX 20-MAY-1998 (first entry)
DT
XX
XX Hypercalcaemia agent portion 2.
DE
XX
XX Antihuman parathyroid hormone-related protein: monoclonal antibody;
KW variable region; rodent/human chimeric MAb; constant region; PTHrP.
XX
XX Synthetic.
OS
XX JP04228089-A.
FN
XX
XX 18-AUG-1992.
PD
XX
XX 15-MAY-1991; 91JP-0110565.
PF
XX
XX 15-MAY-1990; 90JP-0124581.
PR
XX
XX (KANF) KANAKA CORP.
PA
XX
XX WPI: 1992-320987/39.
DR
XX
XX Treatment and preventive agent for hypercalcaemia - contg. one of
PT anti-human para-thyroid-hormone-related protein monoclonal antibody,
PT a rodent or chimera monoclonal antibody, fused gene and cell
PT line, etc.
XX
XX Disclosure; Page 13; 18pp; Japanese.
PS
XX
XX The sequences given in AAR27008-11 are fragments which were used in
CC the construction of an agent for the treating and prevention of

CC hypercalcaemia. The agent contained a portion of the antihuman
 CC parathyroid hormone-related protein monoclonal antibody (antihuman
 CC PTHrP Mab). The Mab was used as the active component in the agent.
 CC The agent further comprises a rodent/human chimeric Mab which has a
 CC rodent variable region and a human constant region and recognises
 CC human PTHrP.
 CC XX
 SO Sequence 92 AA:

Query Match 100.0%; Score 33; DB 13; Length 92;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
 |||||
 DB 68 ftlkisr 74

RESULT 6

AA55670
 ID AAY56670 standard; protein; 93 AA.

XX
 AC AAY56670;

XX
 DT 15-FEB-2000 (first entry)

XX DE Partial peptide fragment of Cynomologous V kappa cDNA clone 4-5.

XX KW Complementarily determining region; antibody; primate; immunogenicity;

XX KM Old World ape; Old World monkey; antigen-binding affinity.

XX OS Macaca cynomolgus.

XX PN WO955369-A1.

XX PD 04-NOV-1999.

XX PF 28-APR-1999; 99WO-US09131.

XX PR 28-APR-1998; 98US-0083367.

XX PA (SMK) SMITHKLINE BEECHAM CORP.

XX PI Taylor AH;

XX DR WPI; 2000-023265/02.

XX DR N-PSDB; AA239338.

XX PT Antibodies containing donor complementarily determining regions and
 PT non-human primate acceptor frameworks, having reduced immunogenicity in
 PT humans -

XX PS Claim 26; Page 101; 123pp; English.

XX CC The invention provides an antibody (Ab) comprising donor CDRs
 CC (complementarily determining regions) derived from a non-human antigen-
 CC specific donor antibody, and an acceptor framework from a non-human
 CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
 CC specific donor antibody onto homologous Old World ape or monkey acceptor
 CC frameworks. The Abs have reduced immunogenicity and are better tolerated
 CC in humans (because of the close similarity between the human and primate
 CC proteins), but retain the full antigen-binding affinity of the donor
 CC antibody.
 CC XX

SO Sequence 93 AA:

Query Match 100.0%; Score 33; DB 21; Length 93;
 Best Local Similarity 100.0%; Pred. No. 3.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7

DB |||||
 76 ftlkisr 82

RESULT 7
 AAR72067
 ID AAR72067 standard; protein; 100 AA.

XX
 AC AAR72067;

XX DT 26-SEP-1995 (first entry)

XX DE Oe7K.7 VK-2 L chain.

XX KM Graves ophthalmopathy associated immunoglobulin protein;

XX KW orbital antigen; monoclonal antibody; light chain; L chain;

XX KM variable region; autoimmunity.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT 23..38 /label= CDR1

XX FT 54..60 /label= CDR2

XX FT 93..100 /label= CDR3

XX PN WO9508336-A.

XX PD 30-MAR-1995.

XX PF 22-SEP-1994; 94WO-US10756.

XX PR 22-SEP-1993; 93US-0124469.

XX PA (NICH-) NICHOLS INST DIAGNOSTICS.

XX PI McIachlan SM, Rapoport B;

XX DR WPI; 1995-139383/18.

XX DR N-PSDB; AA089326.

XX PT Graves' ophthalmopathy-associated monoclonal antibody - produced
 PT by molecular cloning of immunoglobulin genes by PCR

XX PS Claim 4; Page 66; 94pp; English.

XX CC L- and H-chain DNA was amplified by PCR from Graves' orbital
 CC tissue and clones encoding autoimmune-associated immunoglobulin
 CC fragments were obtained. 14/15 clones of L chain (kappa) regions
 CC showed homology to the putative VK germ-line gene KI012 (given in
 CC AA089317) and the remaining clone, Oe7K.7 (AA089326), to the VK005
 CC gene.
 CC XX

SO Sequence 100 AA:

Query Match 100.0%; Score 33; DB 16; Length 100;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
 |||||
 DB 76 ftlkisr 82

RESULT 8

AAR72066
 ID AAR72066 standard; protein; 100 AA.

XX
 AC AAR72066;

XX

```

DT 26-SEP-1995 (first entry)
XX
DE VK005 VK region.
XX
KM Graves ophthalmopathy associated immunoglobulin protein;
KM orbital antigen; monoclonal antibody; light chain; L chain;
KM variable region; autoimmunity.
XX
OS Homo sapiens.
XX
FH Key
FH Region 23..38
FT /label= CDR1
FT Region 54..60
FT /label= CDR2
FT Region 93..100
FT /label= CDR3
XX
PN MO9508336-A.
XX
PD 30-MAR-1995.
XX
PF 22-SEP-1994; 94MO-US10756.
XX
PR 22-SEP-1993; 93US-0124469.
XX
PA (NICH-) NICHOLS INST DIAGNOSTICS.
XX
PI McIachlan SM, Rapoport B;
XX
DR WPI; 1995-139383/18.
DR N-PSDB; AA089325.
XX
PT Graves' ophthalmopathy-associated monoclonal antibody - produced
PT by molecular cloning of immunoglobulin genes by PCR
XX
PS Disclosure: Page 67; 94pp; English.
XX
CC L- and H-chain DNA was amplified by PCR from Graves' orbital
CC tissue and clones encoding autoimmune-associated immunoglobulin
CC fragments were obtained. 14/15 clones of L chain (kappa) regions
CC showed homology to the putative VK germline gene K1012 (given in
CC AA089317) and the remaining clone, OE7K.7 (AA089326), to the VK005
CC gene.
XX
SQ Sequence 100 AA;

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Query Match 100.0%; Score 33; DB 16; Length 100;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 FTLKISR 7
   |||||
DB 76 ftklksr 82

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RESULT 9
 ID AAE12711 standard; peptide; 100 AA.
 AC AAE12711;
 DT 04-JAN-2002 (first entry)
 DE Antibody variable light chain region (VL) from DP47 germ line.
 XX
 KM Tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VL;
 KM variable light chain region; cancer; breast; lung; bladder;
 KM cytostatic; therapy.
 XX
 OS Unidentified.

```

PN MO200175110-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001MO-US10589.
XX
PR 30-MAR-2000; 2000US-0538913.
XX
PA (DYAX-) DYAX CORP.
XX
PI Hoogenboom HRJM, Henderikx MEG;
XX
DR WPI; 2001-626437/72.
XX
PT Novel isolated tumor-associated antigen mucin-1-specific binding member
PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
PT its portion for binding to an epitope of the protein core of mucin-1.
XX
PS Example 1; Page 35; 126pp; English.
XX
CC The invention relates to an isolated tumour-associated antigen mucin-1
CC (MUC-1)-specific binding member comprising an antigen binding domain
CC region having an antibody variable light (VL) or heavy (VH) region,
CC or a complementarily determining region (CDR) of VL or VH. MUC1-specific
CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
CC The binding of MUC1-specific binding member to MUC1 is detected by a
CC detection method selected from enzyme-linked immunosorbent assay,
CC magnetic resonance imaging, scintillation counting, and X-ray film.
CC MUC1-specific binding member is useful for treating cancer, preferably
CC adenocarcinoma, in an individual, where the cancer is present in tissue
CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
CC binding member is useful for diagnosing and imaging MUC1-expressing
CC cancer cells and tissues, for purifying or isolating non-glycosylated,
CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
CC containing molecules, and for therapeutically or prophylactically
CC treating cancer. The present sequence is antibody variable light chain
CC region (VL) from DP47 germ line.
XX
SQ Sequence 100 AA;

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Query Match 100.0%; Score 33; DB 22; Length 100;
 Best Local Similarity 100.0%; Pred. No. 4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 FTLKISR 7
   |||||
DB 76 ftklksr 82

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RESULT 10
 ID AAE06958 standard; Protein; 100 AA.
 AC AAE06958;
 DT 16-OCT-2001 (first entry)
 DE Murine 1D9 antibody partial kappa light chain variable (VK) region.
 XX
 KM Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KM neuroprotective; immunosuppressive; human immunodeficiency virus;
 KM HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KM inflammatory disorder; autoimmune disorder; Rheumatoid arthritis; shock;
 KM multiple sclerosis; atherosclerosis; atherosclerosis; stenosis; asthma;
 KM anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KM fibrotic disease; angioplasty; acquired immune deficiency syndrome;
 KM AIDS; inflammatory glomerulopathy; vascular intervention; 1D9 antibody;
 KM neointimal hyperplasia; VK; kappa light chain variable region.
 XX
 OS Mus sp.
 PN MO200157226-A1.

neuroprotective; immunosuppressive; human immunodeficiency virus;
HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
fibrotic disease; angiodysplasia; acquired immune deficiency syndrome;
AIDS; inflammatory glomerulopathy; vascular intervention;
neointimal hyperplasia; VK; kappa light chain variable region.
OS
Mus sp.
XX
XX WO200157226-A1.
XX
XX 09-AUG-2001.
XX
XX 02-FEB-2001; 2001WO-US03537.
XX
XX 03-FEB-2000; 2000US-0497625.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
XX WPI; 2001-488888/53.
XX
XX Humanized immunoglobulin for treating a CC-chemokine receptor
XX 2-mediated disorder in a patient, comprises a binding specificity for
XX CCR2, and a non-human antigen binding region and human Immunoglobulin
XX -
XX
XX Disclosure; Page 148; 183pp; English.
XX
XX The patent discloses a humanised antibody or its antigen-binding
XX fragment, having binding specificity for CC-chemokine receptor 2
XX (CCR2), comprising an antigen binding region of non-human origin
XX and at least a portion of an immunoglobulin of human origin. The
XX humanised antibodies are useful for inhibiting the interaction of
XX a cell expressing CCR2. They are useful for inhibiting or treating
XX HIV infection. The proteins of the invention are useful for inhibiting
XX leukocyte trafficking, for treating CCR2-mediated disorders such as
XX inflammatory disorder, autoimmune disorders such as rheumatoid
XX arthritis and multiple sclerosis, atherogenesis and atherosclerosis,
XX and for inhibiting restenosis. They are useful in therapy or diagnosis,
XX and in the manufacture of a medicament for treating CCR2-mediated
XX disease. They are also useful for treating allergy, anaphylaxis,
XX malignancy, chronic and acute inflammation, histamine and IgE-
XX mediated allergic reaction, shock, stenosis, allograft rejection,
XX fibrotic disease, asthma, inflammatory glomerulopathies, acquired
XX immune deficiency syndrome (AIDS), restenosis associated with vascular
XX intervention, including angiodysplasia and/or stent placement in a mammal.
XX Humanised antibodies are also useful for inhibiting narrowing of the
XX lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
XX a vessel in a mammal, preferably associated with vascular intervention.
XX The present sequence is mouse germline kappa light chain variable
XX (VK) region, 70/1.
XX
XX Sequence 100 AA:
SQ
Query Match 100.0%; Score 33; DB 22; Length 100;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 FTLKISR 7
| | | | | | |
| | | | | | |
Db 76 ftklksr 82
RESULT 13
AAE06961
ID AAE06961 standard: Protein; 100 AA.
XX
AC AAE06961;

XX
DT 16-OCT-2001 (first entry)
XX
DE Mouse germline kappa light chain variable (VK) region, 70/2.
XX
XX Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
XX neuroprotective; immunosuppressive; human immunodeficiency virus;
XX HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
XX inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
XX multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
XX anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
XX fibrotic disease; angiodysplasia; acquired immune deficiency syndrome;
XX AIDS; inflammatory glomerulopathy; vascular intervention;
XX neointimal hyperplasia; VK; kappa light chain variable region.
XX
OS
Mus sp.
XX
XX
XX Key Location/Qualifiers
XX
XX MISC-difference 7 /label= Unknown
XX
XX WO200157226-A1.
XX
XX 09-AUG-2001.
XX
XX 02-FEB-2001; 2001WO-US03537.
XX
XX 03-FEB-2000; 2000US-0497625.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
XX WPI; 2001-488888/53.
XX
XX Humanized immunoglobulin for treating a CC-chemokine receptor
XX 2-mediated disorder in a patient, comprises a binding specificity for
XX CCR2, and a non-human antigen binding region and human Immunoglobulin
XX -
XX
XX Disclosure; Page 148; 183pp; English.
XX
XX The patent discloses a humanised antibody or its antigen-binding
XX fragment, having binding specificity for CC-chemokine receptor 2
XX (CCR2), comprising an antigen binding region of non-human origin
XX and at least a portion of an immunoglobulin of human origin. The
XX humanised antibodies are useful for inhibiting the interaction of
XX a cell expressing CCR2. They are useful for inhibiting or treating
XX HIV infection. The proteins of the invention are useful for inhibiting
XX leukocyte trafficking, for treating CCR2-mediated disorders such as
XX inflammatory disorder, autoimmune disorders such as rheumatoid
XX arthritis and multiple sclerosis, atherogenesis and atherosclerosis,
XX and for inhibiting restenosis. They are useful in therapy or diagnosis,
XX and in the manufacture of a medicament for treating CCR-2 mediated
XX disease. They are also useful for treating allergy, anaphylaxis,
XX malignancy, chronic and acute inflammation, histamine and IgE-
XX mediated allergic reaction, shock, stenosis, allograft rejection,
XX fibrotic disease, asthma, inflammatory glomerulopathies, acquired
XX immune deficiency syndrome (AIDS), restenosis associated with vascular
XX intervention, including angiodysplasia and/or stent placement in a mammal.
XX Humanised antibodies are also useful for inhibiting narrowing of the
XX lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
XX a vessel in a mammal, preferably associated with vascular intervention.
XX The present sequence is mouse germline kappa light chain variable
XX (VK) region, 70/2.
XX
XX Sequence 100 AA:
SQ
Query Match 100.0%; Score 33; DB 22; Length 100;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
|||||||
Db 76 ftklstr 82

RESULT 14
AAE06962
ID AAE06962 standard; Protein: 100 AA.
XX
XX AAE06962;
XX
DT 16-OCT-2001 (first entry)
DE Mouse germline kappa light chain variable (VK) region, V-IB.
XX
XX Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
KM neuroprotective; immunosuppressive; human immunodeficiency virus;
KM HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
KM inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
KM multiple sclerosis; atherosclerosis; stenosis; allograft rejection;
KM anaphylaxis; malignancy; inflammation; stenosis; restenosis; asthma;
KM fibrotic disease; angiodysplasia; acquired immune deficiency syndrome;
KM AIDS; inflammatory glomerulopathy; vascular intervention;
KM neointimal hyperplasia; VK; kappa light chain variable region.
XX
XX Mus sp.
XX
XX WO200157226-A1.
XX
XX PD 09-AUG-2001.
XX
XX PF 02-FEB-2001; 2001WO-US03537.
XX
XX PR 03-FEB-2000; 2000US-0497625.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
XX
XX DR WPI: 2001-488888/53.
XX
XX PT Humanized immunoglobulin for treating a CC-chemokine receptor
PT 2-mediated disorder in a patient, comprises a binding specificity for
PT CCR2, and a non-human antigen binding region and human immunoglobulin
PT
XX
XX PS Disclosure: Page 148-149; 183pp; English.
XX
XX The patent discloses a humanised antibody or its antigen-binding
CC fragment, having binding specificity for CC-chemokine receptor 2
CC (CCR2), comprising an antigen binding region of non-human origin
CC and at least a portion of an immunoglobulin of human origin. The
CC humanised antibodies are useful for inhibiting the interaction of
CC a cell expressing CCR2. They are useful for inhibiting or treating
CC HIV infection. The proteins of the invention are useful for inhibiting
CC leukocyte trafficking, for treating CCR2-mediated disorders such as
CC inflammatory disorder, autoimmune disorders such as rheumatoid
CC arthritis and multiple sclerosis, atherosclerosis and atherosclerosis,
CC and for inhibiting restenosis. They are useful in therapy or diagnosis,
CC and in the manufacture of a medicament for treating CCR-2 mediated
CC disease. They are also useful for treating allergy, anaphylaxis,
CC malignancy, chronic and acute inflammation, histamine and IgE-
CC mediated allergic reaction, shock, stenosis, allograft rejection,
CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
CC immune deficiency syndrome (AIDS), restenosis associated with vascular
CC intervention, including angiodysplasia and/or stent placement in a mammal.
CC Humanised antibodies are also useful for inhibiting narrowing of the
CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
CC a vessel in a mammal, preferably associated with vascular intervention.
CC The present sequence is mouse germline kappa light chain variable
CC (VK) region, V-IB.
XX
XX Sequence 100 AA;
SQ

Query Match 100.0%; Score 33; DB 22; Length 100;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
|||||||
Db 76 ftklstr 82

RESULT 15
AAE06963
ID AAE06963 standard; Protein: 100 AA.
XX
XX AAE06963;
XX
DT 16-OCT-2001 (first entry)
DE Mouse germline kappa light chain variable (VK) region, V-IC.
XX
XX Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
KM neuroprotective; immunosuppressive; human immunodeficiency virus;
KM HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
KM inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
KM multiple sclerosis; atherosclerosis; stenosis; restenosis; asthma;
KM anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
KM fibrotic disease; angiodysplasia; acquired immune deficiency syndrome;
KM AIDS; inflammatory glomerulopathy; vascular intervention;
KM neointimal hyperplasia; VK; kappa light chain variable region.
XX
XX Mus sp.
XX
XX WO200157226-A1.
XX
XX PD 09-AUG-2001.
XX
XX PF 02-FEB-2001; 2001WO-US03537.
XX
XX PR 03-FEB-2000; 2000US-0497625.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
XX
XX DR WPI: 2001-488888/53.
XX
XX PT Humanized immunoglobulin for treating a CC-chemokine receptor
PT 2-mediated disorder in a patient, comprises a binding specificity for
PT CCR2, and a non-human antigen binding region and human immunoglobulin
PT
XX
XX PS Disclosure: Page 149; 183pp; English.
XX
XX The patent discloses a humanised antibody or its antigen-binding
CC fragment, having binding specificity for CC-chemokine receptor 2
CC (CCR2), comprising an antigen binding region of non-human origin
CC and at least a portion of an immunoglobulin of human origin. The
CC humanised antibodies are useful for inhibiting the interaction of
CC a cell expressing CCR2. They are useful for inhibiting or treating
CC HIV infection. The proteins of the invention are useful for inhibiting
CC leukocyte trafficking, for treating CCR2-mediated disorders such as
CC inflammatory disorder, autoimmune disorders such as rheumatoid
CC arthritis and multiple sclerosis, atherosclerosis and atherosclerosis,
CC and for inhibiting restenosis. They are useful in therapy or diagnosis,
CC and in the manufacture of a medicament for treating CCR-2 mediated
CC disease. They are also useful for treating allergy, anaphylaxis,
CC malignancy, chronic and acute inflammation, histamine and IgE-
CC mediated allergic reaction, shock, stenosis, allograft rejection,
CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
CC immune deficiency syndrome (AIDS), restenosis associated with vascular
CC intervention, including angiodysplasia and/or stent placement in a mammal.
CC Humanised antibodies are also useful for inhibiting narrowing of the

CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
CC a vessel in a mammal, preferably associated with vascular intervention.
CC The present sequence is mouse germline kappa light chain variable
CC (VK) region, V-IC.
XX
SQ Sequence 100 AA:

Query Match 100.0%; Score 33; DB 22; Length 100;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
|||
Db 76 ftlKISR 82

Search completed: July 15, 2002, 12:57:58
Job time: 414 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 12:59:18 ; Search time 75.67 seconds
(without alignments)
2.260 Million cell updates/sec

Title: US-09-712-819A-6

Perfect score: 33

Sequence: 1 FTLKISR 7

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008
Listing first 45 summaries

Database :

Issued Patents,AA:*
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2: /cgn2_6/pdata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/pdata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/pdata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/pdata/2/1aa/PCUS.COMB.pep.*
6: /cgn2_6/pdata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	32	1	US-08-477-877B-33
2	33	100.0	32	1	US-07-977-696C-71
3	33	100.0	32	1	US-08-129-930B-71
4	33	100.0	32	2	US-08-472-281A-33
5	33	100.0	32	2	US-08-477-969B-33
6	33	100.0	32	4	US-08-976-288A-71
7	33	100.0	81	1	US-08-497-312-19
8	33	100.0	104	3	US-08-881-037-37
9	33	100.0	108	1	US-08-488-113B-151
10	33	100.0	108	1	US-08-477-484B-151
11	33	100.0	108	1	US-08-107-669D-15
12	33	100.0	108	1	US-08-472-788A-15
13	33	100.0	108	2	US-08-477-531B-15
14	33	100.0	108	2	US-08-646-360-151
15	33	100.0	108	2	US-08-082-842A-15
16	33	100.0	108	2	US-08-378-939-22
17	33	100.0	108	2	US-08-378-939-28
18	33	100.0	108	2	US-08-378-939-30
19	33	100.0	108	4	US-08-839-765-151
20	33	100.0	108	4	US-09-136-389-151
21	33	100.0	110	1	US-08-244-626-2
22	33	100.0	111	1	US-07-942-245-29
23	33	100.0	112	1	US-08-053-171-15
24	33	100.0	112	1	US-08-053-171-16
25	33	100.0	112	1	US-08-331-398A-48
26	33	100.0	112	1	US-08-331-398A-49
27	33	100.0	112	1	US-08-331-398A-50

28	33	100.0	112	1	US-07-942-245-28	Sequence 28, Appl
29	33	100.0	112	1	US-08-478-039-88	Sequence 88, Appl
30	33	100.0	112	1	US-08-478-039-89	Sequence 89, Appl
31	33	100.0	112	1	US-08-477-877B-89	Sequence 89, Appl
32	33	100.0	112	1	US-08-077-252B-3	Sequence 3, Appl1
33	33	100.0	112	1	US-08-476-349A-88	Sequence 88, Appl1
34	33	100.0	112	1	US-08-476-349A-89	Sequence 89, Appl1
35	33	100.0	112	1	US-08-388-672A-25	Sequence 25, Appl
36	33	100.0	112	2	US-08-475-000-18	Sequence 18, Appl
37	33	100.0	112	2	US-08-472-281A-89	Sequence 89, Appl
38	33	100.0	112	2	US-08-483-199-18	Sequence 18, Appl
39	33	100.0	112	2	US-08-859-649-19	Sequence 19, Appl
40	33	100.0	112	2	US-08-859-649-29	Sequence 29, Appl
41	33	100.0	112	2	US-08-606-293-4	Sequence 4, Appl1
42	33	100.0	112	2	US-08-606-293-8	Sequence 8, Appl1
43	33	100.0	112	2	US-08-678-194-6	Sequence 6, Appl1
44	33	100.0	112	2	US-08-752-844-15	Sequence 15, Appl
45	33	100.0	112	2	US-08-484-508-18	Sequence 18, Appl

ALIGNMENTS

```
RESULT 1
US-08-477-877B-33
Sequence 33, Application US/08477877B
Patent No. 5730979
GENERAL INFORMATION:
APPLICANT: Bazin, Herv
TITLE OF INVENTION: Latrine, Dominique
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSER: Carella, Byrne, Bain, Gilfillan,
ADDRESSER: Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477, 877B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407, 009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119, 032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027, 008
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24, 025
REFERENCE/DOCKET NUMBER: 61750-146
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
US-08-477-877B-33
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Query Match 100.0%; Score 33; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
DB 15 FTLKISR 21

RESULT 2
US-07-977-696C-71

; Sequence 71, Application US/07977696C
; Patent No. 5792852

; GENERAL INFORMATION:

; APPLICANT: do Couto, Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.

; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padian Dr., Eduardo A.

; TITLE OF INVENTION: Analogue Peptides with Specificity
; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination

; NUMBER OF SEQUENCES: 81
; THERAPEUTIC METHODS:

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI

; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles

; STATE: California
; COUNTRY: USA

; ZIP: 90071

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0

; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/977,696C
; FILING DATE: 11-16-92

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930

; REFERENCE/DOCKET NUMBER: P66 38227
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (510) 748-6868
; TELEFAX: (510) 748-6868

; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 71:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids

; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-07-977-696C-71

Query Match 100.0%; Score 33; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
DB 15 FTLKISR 21

RESULT 3
US-08-129-930B-71

; Sequence 71, Application US/08129930B
; Patent No. 5804187

; GENERAL INFORMATION:

; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.

; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padian Dr., Eduardo A.

; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods

; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187ch Broadway, Suite 201

; CITY: Walnut Creek
; STATE: California

; COUNTRY: USA
; ZIP: 94596

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0

; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/129,930B
; FILING DATE: September 30, 1993

; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:

; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930

; REFERENCE/DOCKET NUMBER: CRCC-008A
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (510) 521-1333
; TELEFAX: (510) 521-3541

; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 71:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids

; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-08-129-930B-71

Query Match 100.0%; Score 33; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
DB 15 FTLKISR 21

RESULT 4
US-08-472-281A-33

; Sequence 33, Application US/08472281A
; Patent No. 5817311

; GENERAL INFORMATION:

; APPLICANT: Bazin, Herv
; TITLE OF INVENTION: Latrine, Dominique

; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cecchi, Byrne, Bain, Gilfillan,
; STREET: 6 Becker Farm Road

; CITY: Roseland
; STATE: New Jersey

; COUNTRY: U.S.A.
; ZIP: 07068

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette

; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/472,281A
; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 05-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
US-08-472-281a-33

Query Match 100.0%; Score 33; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
|||||
Db 15 FTLKISR 21

RESULT 5
US-08-477-989B-33
Sequence 33, Application US/08477989B
Patent No. 5951983
GENERAL INFORMATION:
APPLICANT: Bazin, Herv
APPLICANT: Latime, Dominique
APPLICANT: Kaplan, Ruth
APPLICANT: Kieber-Emmons, Thomas
APPLICANT: Postema, Christina E.
APPLICANT: White-Scharf, Mary
TITLE OF INVENTION: LO-CD2a Antibody and Uses
TITLE OF INVENTION: Therect for inhibiting
TITLE OF INVENTION: T-Cell Activation and
TITLE OF INVENTION: Proliferation
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gillfillan,
ADDRESSEE: Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,989B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,009
FILING DATE: 29-MAR-1995
APPLICATION NUMBER: 08/119,032
FILING DATE: 09-SEP-1993
APPLICATION NUMBER: 08/027,008
FILING DATE: 05-MAR-1993

ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 61750-147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
US-08-477-989B-33

Query Match 100.0%; Score 33; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
|||||
Db 15 FTLKISR 21

RESULT 6
US-08-976-288a-71
Sequence 71, Application US/08976288A
Patent No. 6315997
GENERAL INFORMATION:
APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: Ceriani Dr., Roberto L.
APPLICANT: Peterson Dr., Jerry A.
APPLICANT: Padian Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
TITLE OF INVENTION: Carcinoma Specificity, and Kit and
TITLE OF INVENTION: Diagnostic Vaccination and
TITLE OF INVENTION: Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty Schroeder & Poplawski
STREET: 444 South Flower St., 19th floor
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,288A
FILING DATE: No. 6315997ember 21, 1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/129,930
FILING DATE: September 30, 1993
APPLICATION NUMBER: 07/977,696
FILING DATE: No. 6315997ember 16, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel Ph.D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P663938
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
TELEX: n.a.
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-976-288A-71

Query Match 100.0%; Score 33; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
|||||
DB 15 FTLKISR 21

RESULT 7
US-08-497-312-19
Sequence 19, Application US/08497312
Patent No. 5712120
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Method for obtaining modified
TITLE OF INVENTION: Immunoglobulins with reduced immunogenicity of murine
TITLE OF INVENTION: antibody variable domains, compositions containing them.
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: CENTRO DE INMUNOLOGIA MOLECULAR
STREET: 215 Y 15, ATABEY PLAYA
CITY: HAVANA
STATE:
COUNTRY: CUBA
ZIP: 11600
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/497.312
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CU 80/94
FILING DATE: 30-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: BOND, LAURENCE B.
REGISTRATION NUMBER: 30,549
REFERENCE/DOCKET NUMBER: 2629US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 801/532-1922
TELEFAX: 801/531-9168
TELEX: 388961 IPMDUT
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 81 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-497-312-19

Query Match 100.0%; Score 33; DB 1; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
|||||
DB 53 FTLKISR 59

RESULT 8
US-08-881-037-37

Sequence 37, Application US/08881037
Patent No. 6080568
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881.037
FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kanski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX:
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-881-037-37

Query Match 100.0%; Score 33; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
|||||
DB 68 FTLKISR 74

RESULT 9
US-08-488-113B-151
Sequence 151, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studinka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-488-113B-151

Query Match 100.0%; Score 33; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
Db 72 FTLKISR 78

RESULT 10
US-08-477-484B-151
Sequence 151, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Catrall, Stephen F.
APPLICANT: Studinka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B

FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-477-484B-151

Query Match 100.0%; Score 33; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 FTLKISR 7
Db 72 FTLKISR 78

RESULT 11
US-08-107-669D-15
Sequence 15, Application US/08107669D
Patent No. 5766886
GENERAL INFORMATION:
APPLICANT: Studinka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,669D
FILING DATE: 13-AUG-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991

ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbalia
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000001/MAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-107-669d-15

Query Match 100.0%; Score 33; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
DB 72 FTLKISR 78

RESULT 12
US-08-472-788A-15
Sequence 15, Application US/08472788A
Patent No. 5770196
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,788A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/082,842
FILING DATE: 23-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cimbalia, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-472-788A-15

Query Match 100.0%; Score 33; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
DB 72 FTLKISR 78

RESULT 13
US-08-477-531B-15
Sequence 15, Application US/08477531B
Patent No. 5821123
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,531B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/107,669
FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbalia
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-531B-15

Query Match 100.0%; Score 33; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTLKISR 7
DB 72 FTLKISR 78

RESULT 14
US-08-646-360-151
Sequence 151, Application US/08646360
Patent No. 5837491

GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-646-360-151

Query Match 100.0%; Score 33; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
Db 72 FTLKISR 78

RESULT 15
US-08-082-842a-15
Sequence 15, Application US/08082842a
Patent No. 5869619
GENERAL INFORMATION:
APPLICANT: Studnicka, Gary M.
TITLE OF INVENTION: Modified Antibody Variable Domains
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,842a
FILING DATE: 23-JUN-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Climbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-082-842a-15

Query Match 100.0%; Score 33; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTLKISR 7
Db 72 FTLKISR 78

Search completed: July 15, 2002, 12:59:19
Job time: 390 sec

GenCore version 4.5
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OK protein - protein search, using sw model

Run on: July 15, 2002, 13:01:01 ; Search time 95.45 Seconds
(without alignments)
9.060 Million cell updates/sec

Title: US-09-712-819A-7

Perfect score: 43

Sequence: 1 TDFLTRISS 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	54	2 JT0521	Ig kappa chain V-I
2	43	100.0	71	2 S21526	Ig kappa chain V-I
3	43	100.0	78	2 S34102	Ig kappa chain V-I
4	43	100.0	79	2 S24215	Ig kappa chain V-I
5	43	100.0	81	2 PH1048	Ig light chain V-I
6	43	100.0	86	2 S16826	Ig kappa chain V-I
7	43	100.0	86	2 S16834	Ig kappa chain V-I
8	43	100.0	86	2 S16836	Ig kappa chain V-I
9	43	100.0	86	2 S34086	Ig kappa chain V-I
10	43	100.0	86	2 S16840	Ig kappa chain V-I
11	43	100.0	86	2 S16837	Ig kappa chain V-I
12	43	100.0	86	2 S16833	Ig kappa chain V-I
13	43	100.0	86	2 S16830	Ig kappa chain V-I
14	43	100.0	86	2 S16824	Ig kappa chain V-I
15	43	100.0	86	2 S16829	Ig kappa chain V-I
16	43	100.0	87	2 S34084	Ig kappa chain V-I
17	43	100.0	87	2 S34083	Ig kappa chain V-I
18	43	100.0	88	2 S21528	Ig kappa chain V-I
19	43	100.0	88	2 S21525	Ig kappa chain V-I
20	43	100.0	88	2 S21522	Ig kappa chain V-I
21	43	100.0	91	2 PH1071	Ig light chain V-I
22	43	100.0	91	2 S37521	Ig kappa chain V-I
23	43	100.0	92	2 S37533	Ig kappa chain V-I
24	43	100.0	92	2 S37530	Ig kappa chain V-I
25	43	100.0	92	2 S37529	Ig kappa chain V-I
26	43	100.0	92	2 S37535	Ig kappa chain V-I
27	43	100.0	92	2 S37512	Ig kappa chain V-I
28	43	100.0	92	2 S37531	Ig kappa chain V-I
29	43	100.0	92	2 S37534	Ig kappa chain V-I

30	43	100.0	92	2 S37532	Ig kappa chain V-I
31	43	100.0	92	2 S37516	Ig kappa chain V-I
32	43	100.0	92	2 S37522	Ig kappa chain V-I
33	43	100.0	92	2 S37506	Ig kappa chain V-I
34	43	100.0	92	2 S37504	Ig kappa chain V-I
35	43	100.0	94	2 S20648	Ig heavy chain V-I
36	43	100.0	95	2 PH0863	Ig kappa chain V-I
37	43	100.0	95	2 PH0867	Ig kappa chain V-I
38	43	100.0	96	2 PH1070	Ig light chain V-I
39	43	100.0	96	2 S38601	Ig kappa chain V-I
40	43	100.0	96	2 S45441	Ig kappa chain V-I
41	43	100.0	97	2 A42375	Ig kappa chain V-I
42	43	100.0	98	2 PH1066	Ig light chain V-I
43	43	100.0	98	2 PH1067	Ig light chain V-I
44	43	100.0	98	2 PH1083	Ig light chain V-I
45	43	100.0	98	2 S19974	Ig kappa chain V-I

ALIGNMENTS

RESULT 1
JT0521
Ig kappa chain V-III region (CPI) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 23-Oct-1992 #sequence_revision 23-Oct-1992 #text_change 09-May-1997
R:Accession: JT0521
R:Anker, R.; Conley, M.E.; Pollok, B.A.
J. Exp. Med. 169, 2109-2119, 1989
A:Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobulinemia
A:Reference number: JT0511; MUID:89279157
A:Accession: JT0521
A:Molecule type: mRNA
A:Residues: 1-54 <ANK>
A>Note: the sequence shown here is one of eight productive V-D-J mu chain rearrangements
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:1-49/Domain: V region <VRE>
F:50-54/Domain: J region <JRE>

Query Match 100.0%; Score 43; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTRISS 9
DB 21 TDFLTRISS 29

RESULT 2
S21526
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 23-Jul-1999
C:Accession: S34082; S21526
R:Magner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387
A:Accession: S34082
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-71 <MA2>
A:Cross-references: EMBL:X66042; NID:933318; PIDN:CAA46841.1; PID:933319
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match 100.0%; Score 43; DB 2; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TDFLTRISS 9
|||||
Db 62 TDFLTRISS 70

RESULT 3

S34102
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 07-May-1999
C:Accession: S34102
R:Magner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387
A:Accession: S34102
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-78 <MAC>
A:Cross-references: EMBL:X67186
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 43; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TDFLTRISS 9
|||||
Db 60 TDFLTRISS 68

RESULT 4

S24215
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S24215
R:Shimizu, T.; Iwasato, T.; Yamagishi, H.
J. Exp. Med. 173, 1065-1072, 1991
A:Title: Deletions of immunoglobulin C(kappa) region characterized by the circular excise
A:Reference number: S24214; MUID:91217618
A:Accession: S24215
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-79 <SHL>
A:Cross-references: EMBL:X58202; NID:953718; PIDN:CAA41178.1; PID:930195
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 43; DB 2; Length 79;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TDFLTRISS 9
|||||
Db 42 TDFLTRISS 50

RESULT 5

PH1048
Ig light chain V region (clone 165.49) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C:Accession: PH1048
R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B
A:Reference number: PH0571; MUID:9238144
A:Accession: PH1048
A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-81 <TIL>
A:Experimental source: B cell, strain (NZB x NZW)F1
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 100.0%; Score 43; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TDFLTRISS 9
|||||
Db 54 TDFLTRISS 62

RESULT 6

S16826
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16826; S34101
R:Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid
A:Reference number: S16823; MUID:91243737
A:Accession: S16826
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BIA>
A:Cross-references: EMBL:X54824; NID:933653; PIDN:CAA38593.1; PID:933654
R:Magner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distrib
A:Reference number: S34076; MUID:93170387
A:Accession: S34101
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-86 <MAC>
A:Cross-references: EMBL:X67185
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 43; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TDFLTRISS 9
|||||
Db 60 TDFLTRISS 68

RESULT 7

S16834
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16834
R:Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid
A:Reference number: S16823; MUID:91243737
A:Accession: S16834
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BIA>
A:Cross-references: EMBL:X54832
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 43; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TDFLTITSS 9
|||||
Db 60 TDFLTITSS 68

RESULT 8
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16836
R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A:Reference number: S16823; MUID:91243737
A:Accession: S16836
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54834
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 43; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TDFLTITSS 9
|||||
Db 60 TDFLTITSS 68

RESULT 9
S34086
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S34086
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387
A:Accession: S34086
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-86 <NAG>
A:Cross-references: EMBL:X67169
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:9-83/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 43; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TDFLTITSS 9
|||||
Db 62 TDFLTITSS 70

RESULT 10
S16840
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S16840
R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid
A:Reference number: S16823; MUID:91243737
A:Accession: S16840
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54838
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 43; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TDFLTITSS 9
|||||
Db 60 TDFLTITSS 68

RESULT 11
S16837
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16837
R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid
A:Reference number: S16823; MUID:91243737
A:Accession: S16837
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54835
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 43; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TDFLTITSS 9
|||||
Db 60 TDFLTITSS 68

RESULT 12
S16833
Ig kappa chain V-III region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16833; S16838
R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid
A:Reference number: S16823; MUID:91243737
A:Accession: S16833
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLA>
A:Cross-references: EMBL:X54831
A:Experimental source: clone Bkv17
A:Accession: S16838
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-86 <BLM>

A:Cross-references: EMBL:X54836
 A:Experimental source: clone s1kv14
 C:Superfamily: Immunoglobulin V region: immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 43; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 0.071;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TDFLTITSS 9
 |||||||||
 DB 60 TDFLTITSS 68

RESULT 13
 S16830
 Ig kappa chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S16830
 R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
 Eur. J. Immunol. 21, 1221-1227, 1991
 A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
 A:Reference number: S16823; MUID:91243737
 A:Accession: S16830
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-86 <BLA>
 A:Cross-references: EMBL:X54828
 C:Superfamily: immunoglobulin V region: immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 43; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 0.071;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTITSS 9
 |||||||||
 DB 60 TDFLTITSS 68

RESULT 14
 S16824
 Ig kappa chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S16824
 R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
 Eur. J. Immunol. 21, 1221-1227, 1991
 A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
 A:Reference number: S16823; MUID:91243737
 A:Accession: S16824
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-86 <BLA>
 A:Cross-references: EMBL:X54822
 C:Superfamily: immunoglobulin V region: immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 43; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 0.071;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTITSS 9
 |||||||||
 DB 60 TDFLTITSS 68

RESULT 15
 S16829
 Ig kappa chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S16829
 R:Blaisson, G.; Kuntz, J.L.; Pasquali, J.L.
 Eur. J. Immunol. 21, 1221-1227, 1991
 A:Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid
 A:Reference number: S16823; MUID:91243737
 A:Accession: S16829
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-86 <BLA>
 A:Cross-references: EMBL:X54827
 C:Superfamily: immunoglobulin V region: immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 43; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 0.071;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTITSS 9
 |||||||||
 DB 60 TDFLTITSS 68

Search completed: July 15, 2002, 13:01:02
 Job time: 468 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 13:23:33 ; Search time 44.9 Seconds

(without alignments)
7.761 Million cell updates/sec

Title: US-09-712-819A-7

Sequence: 1 TDFLTITSS 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt-40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	43	100.0	107 1	KVID_HUMAN P01596 homo sapien
2	43	100.0	108 1	KVID_HUMAN P01600 homo sapien
3	43	100.0	108 1	KV5Q_MOUSE P01650 mus musculu
4	43	100.0	108 1	KV5R_MOUSE P01651 mus musculu
5	43	100.0	108 1	KV5S_MOUSE P01652 mus musculu
6	43	100.0	108 1	KV5T_MOUSE P01653 mus musculu
7	43	100.0	109 1	KV1T_HUMAN P01612 homo sapien
8	43	100.0	114 1	KV1A_MOUSE P01632 mus musculu
9	43	100.0	114 1	KV4A_HUMAN P01625 homo sapien
10	43	100.0	115 1	KV3I_HUMAN P04433 homo sapien
11	43	100.0	116 1	KV3J_HUMAN P04434 homo sapien
12	43	100.0	117 1	KV1I_HUMAN P01601 homo sapien
13	43	100.0	121 1	KV4O_HUMAN P06312 homo sapien
14	43	100.0	129 1	KV1W_HUMAN P04313 homo sapien
15	43	100.0	133 1	KV4B_HUMAN P06313 homo sapien
16	43	100.0	134 1	KV4C_HUMAN P06314 homo sapien
17	43	100.0	136 1	KV5B_MOUSE P01634 mus musculu
18	40	93.0	108 1	KV1Q_HUMAN P01609 homo sapien
19	39	90.7	100 1	KV3C_HUMAN P01621 homo sapien
20	39	90.7	107 1	KV04_RABIT P01685 coryctolagus
21	39	90.7	108 1	KV06_RABIT P01687 coryctolagus
22	39	90.7	108 1	KV1E_HUMAN P01597 homo sapien
23	39	90.7	108 1	KV1F_HUMAN P01598 homo sapien
24	39	90.7	108 1	KV1G_HUMAN P01599 homo sapien
25	39	90.7	108 1	KV1M_HUMAN P01605 homo sapien
26	39	90.7	108 1	KV1P_HUMAN P01608 homo sapien
27	39	90.7	108 1	KV1S_HUMAN P01611 homo sapien
28	39	90.7	108 1	KV1Y_HUMAN P01620 homo sapien
29	39	90.7	109 1	KV3B_HUMAN P01622 homo sapien
30	39	90.7	109 1	KV3D_HUMAN P01623 homo sapien
31	39	90.7	109 1	KV3E_HUMAN P01624 homo sapien
32	39	90.7	109 1	KV3F_HUMAN P04206 homo sapien
33	39	90.7	109 1	KV3G_HUMAN P04206 homo sapien

34	39	90.7	117 1	KV1J_HUMAN P01602 homo sapien
35	39	90.7	129 1	KV3L_HUMAN P18135 homo sapien
36	39	90.7	129 1	KV3M_HUMAN P18136 homo sapien
37	39	90.7	149 1	KV5A_MOUSE P01633 mus musculu
38	38	88.4	109 1	KV01_RAT P01681 rattus norv
39	37	86.0	104 1	KV17_RABIT P01698 coryctolagus
40	37	86.0	108 1	KV1K_HUMAN P01603 homo sapien
41	37	86.0	108 1	KV1N_HUMAN P01606 homo sapien
42	37	86.0	108 1	KV1V_HUMAN P04430 homo sapien
43	37	86.0	115 1	KV5A_HUMAN P06315 homo sapien
44	36	83.7	108 1	KV1L_HUMAN P01604 homo sapien
45	36	83.7	108 1	KV1O_HUMAN P01607 homo sapien

ALIGNMENTS

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RESULT 1
KVID_HUMAN STANDARD; PRT; 107 AA.
AC P01596;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, last sequence update)
DE 15-JUL-1999 (Rel. 38, last annotation update)
DE 19 kappa chain V-I region CAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75075135; PubMed=4216454;
RA Milstein C.P., Deverson E.V.;
RT Primary structure of kappa light chain from a human myeloma
RT protein.
RL Eur. J. Biochem. 49:377-391(1974).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
CC PIR: A01864; KIHUAR.
DR HSSP: P80362; 1krt.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Glycoprotein.
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11703 MW; E1BFD0P9844C3346 CRC64;
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Query Match 100.0%; Score 43; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTITSS 9
Db 69 TDFLTITSS 77

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RESULT 2
KVID_HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DE 21-JUL-1986 (Rel. 01, last sequence update)
DE 15-JUL-1999 (Rel. 38, last annotation update)
DE 19 kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
```

RP SEQUENCE:
 RX MEDLINE-71032830; PubMed-4097974;
 RA Watanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
 chain of subgroup I (Bence-Jones Protein Hau); subdivision within
 RT subgroups.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENGE-JONES PROTEIN.
 DR PIR: A01868; K1H0H0.
 DR HSSP: P80362; 1MTL.
 DR InterPro: IPR003006; 1G_MHC.
 DR InterPro: IPR003596; 1G_V.
 DR Pfam: PF00047; 1g; 1.
 DR SMART: SM00406; 1g; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160DBD0618 CRC64;

Query Match 100.0%; Score 43; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
 Db 69 TDFTLTSS 77

RESULT 3
 KVSS_MOUSE STANDARD; PRT; 108 AA.
 ID KVSS_MOUSE
 AC P01650;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 1g kappa chain V-V region UPC 61.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID-10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-79195288; PubMed-109517;
 RA Vrana M., Rudikoff S., Potter M.;
 RT "The structural basis of a hapten-inhibitable kappa-chain idiotype.";
 RL J. Immunol. 122:1905-1910(1979).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
 CC BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
 DR PIR: A01929; KVM561.
 DR HSSP: P80362; 1MTL.
 DR InterPro: IPR003006; 1G_MHC.
 DR InterPro: IPR003596; 1G_V.
 DR Pfam: PF00047; 1g; 1.
 DR SMART: SM00406; 1g; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 106 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108

SQ SEQUENCE 108 AA; 11809 MW; FAE4DA36076F2AFE CRC64;

Query Match 100.0%; Score 43; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
 Db 69 TDFTLTSS 77

RESULT 4
 KVSR_MOUSE STANDARD; PRT; 108 AA.
 ID KVSR_MOUSE
 AC P01651;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 1g kappa chain V-V region EPC 109.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID-10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-79195288; PubMed-109517;
 RA Vrana M., Rudikoff S., Potter M.;
 RT "The structural basis of a hapten-inhibitable kappa-chain idiotype.";
 RL J. Immunol. 122:1905-1910(1979).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
 CC BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
 DR PIR: B92808; KVM509.
 DR HSSP: P01607; 1RET.
 DR InterPro: IPR003006; 1G_MHC.
 DR InterPro: IPR003596; 1G_V.
 DR Pfam: PF00047; 1g; 1.
 DR SMART: SM00406; 1g; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 108 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108
 SQ SEQUENCE 108 AA; 11876 MW; 35C116BD60F79310 CRC64;

Query Match 100.0%; Score 43; DB 1; Length 108;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
 Db 69 TDFTLTSS 77

RESULT 5
 KVSS_MOUSE STANDARD; PRT; 108 AA.
 ID KVSS_MOUSE
 AC P01652;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 1g kappa chain V-V region J606.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID-10090;
 RN [1]

```

RP      SEQUENCE
RX      MEDLINE-82099361; PubMed-6798111;
RA      Johnson N., Slankard J., Paul L., Hood L.;
RT      "The complete V domain amino acid sequences of two myeloma Inulin-
RT      binding proteins."
RL      J. Immunol. 128:302-307(1982).
CC      -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC      BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR      PIR: A92811; KWS06.
DR      HSSP; P01607; IREL.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003596; Ig_V.
DR      Pfam: PF00047; Ig; 1.
DR      SMART: SM00406; IGV; 1.
KV      Immunoglobulin V region.
FT      DOMAIN 1 23
FT      DOMAIN 2 34
FT      DOMAIN 3 49
FT      DOMAIN 4 50
FT      DOMAIN 5 56
FT      DOMAIN 6 57
FT      DOMAIN 7 88
FT      DOMAIN 8 89
FT      DOMAIN 9 97
FT      DOMAIN 10 98
FT      DISULFID 23 88
FT      NON_TER 108
SQ      SEQUENCE 108 AA; 11810 MW; 8D54DD31076F2A2B CRC64;

Query Match 100.0%; Score 43; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 TDFLTITSS 9
DB      69 TDFLTITSS 77

RESULT 6
KVST_MOUSE STANDARD; PRT; 108 AA.
AC      P01653;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig kappa chain V-V region W3082.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE-82099361; PubMed-6798111;
RA      Johnson N., Slankard J., Paul L., Hood L.;
RT      "The complete V domain amino acid sequences of two myeloma Inulin-
RT      binding proteins."
RL      J. Immunol. 128:302-307(1982).
CC      -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT
CC      BIND BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR      PIR: B92811; KWS82.
DR      HSSP; P80362; IWTU.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003596; Ig_V.
DR      Pfam: PF00047; Ig; 1.
DR      SMART: SM00406; IGV; 1.
KV      Immunoglobulin V region.
FT      DOMAIN 1 23
FT      DOMAIN 2 34
FT      DOMAIN 3 49
FT      DOMAIN 4 50
FT      DOMAIN 5 56
FT      DOMAIN 6 57
FT      DOMAIN 7 88
FT      DOMAIN 8 89
FT      DOMAIN 9 97
FT      DOMAIN 10 98
FT      DISULFID 23 88
FT      NON_TER 108
SQ      SEQUENCE 108 AA; 10810 MW; 8D54DD31076F2A2B CRC64;

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SQ      SEQUENCE 108 AA; 11850 MW; C5C145DC376F30CD CRC64;

Query Match 100.0%; Score 43; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 TDFLTITSS 9
DB      69 TDFLTITSS 77

RESULT 7
KVLT_HUMAN STANDARD; PRT; 109 AA.
ID      KVLT_HUMAN
AC      P01612;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig kappa chain V-I region Mev.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE-83081018; PubMed-6816713;
RA      Eullitz M., Linke R.P.;
RT      "Primary structure of the variable part of an amyloidogenic
RT      Bence-Jones Protein (Mev). An unusual insertion in the third
RT      hypervariable region of a human kappa-immunoglobulin light chain."
RL      Hoppe-Seyler's Z. Physiol. Chem. 363:1347-1358(1982).
CC      -1- MISCELLANEOUS: ANOTHER FORM THAT LACKED RESIDUES 1-3 WAS ALSO
CC      FOUND.
CC      -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR      PIR: A01879; KIH0WV.
DR      HSSP; P01730; IWI0.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003596; Ig_V.
DR      Pfam: PF00047; Ig; 1.
DR      SMART: SM00406; IGV; 1.
KV      Immunoglobulin V region.
FT      DOMAIN 1 23
FT      DOMAIN 2 34
FT      DOMAIN 3 49
FT      DOMAIN 4 50
FT      DOMAIN 5 56
FT      DOMAIN 6 57
FT      DOMAIN 7 88
FT      DOMAIN 8 89
FT      DOMAIN 9 98
FT      DOMAIN 10 108
FT      DISULFID 23 88
FT      NON_TER 109
SQ      SEQUENCE 109 AA; 11870 MW; B6ABF451D55F5A0 CRC64;

Query Match 100.0%; Score 43; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 TDFLTITSS 9
DB      69 TDFLTITSS 77

RESULT 8
KVLA_MOUSE STANDARD; PRT; 114 AA.
ID      KVLA_MOUSE
AC      P01632;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig kappa chain V-I region S107A.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=81241357; PubMed=6788890;
RA Kwan S.-P., Rudnikoff S., Seidman J.G., Leder P., Scharff M.D.;
RT "Nucleic acid and protein sequences of phosphocholine-binding light
   chains.";
RL J. Exp. Med. 151:1366-1370(1981).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U28423; AAC00033.1; -
DR PIR: A01915; KVMSTK.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003506; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 41 55 FRAMEWORK-2.
FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 63 94 FRAMEWORK-3.
FT DOMAIN 95 103 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 104 113 FRAMEWORK-4.
FT DISULFID 23 94 BY SIMILARITY.
FT NON_TER 114 114
SO SEQUENCE 114 AA; 12717 MW; 32008EC8E9DEB67B CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 1; Length 114;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFLTITSS 9
DB 75 TDFLTITSS 83

RESULT 9
KV4A_HUMAN STANDARD; PRT; 114 AA.
ID KV4A_HUMAN
AC P01625;
DT 21-JUL-1986 (Rel. 01. Created)
DT 01-OCT-1996 (Rel. 34. Last sequence update)
DT 15-JUL-1999 (Rel. 38. Last annotation update)
DE Ig kappa chain V-IV region Len.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE.
RX MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hilschmann N.;
RT "The primary structure of a monoclonic immunoglobulin-L-chain of
   subunit IV of the kappa type (Bence-Jones protein Len).";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
RN (2)
RP REVISION TO 9.
RA Salomon A.;
RT Submitted (AUG-1996) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01903; KAHUIN.
```

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DR HSSP: P01789; IMCP.
DR InterPro: IPR003506; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 41 55 FRAMEWORK-2.
FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 63 94 FRAMEWORK-3.
FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 113 FRAMEWORK-4.
FT DISULFID 23 94 BY SIMILARITY.
FT NON_TER 114 114
SO SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;

Query Match
Best Local Similarity 100.0%; Score 43; DB 1; Length 114;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFLTITSS 9
DB 75 TDFLTITSS 83

RESULT 10
KV3I_HUMAN STANDARD; PRT; 115 AA.
ID KV3I_HUMAN
AC P04433;
DT 13-AUG-1987 (Rel. 05. Created)
DT 13-AUG-1987 (Rel. 05. Last sequence update)
DT 15-JUL-1999 (Rel. 38. Last annotation update)
DE Ig kappa chain V-III region VG precursor (fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
   within the VK locus.";
RL Nucleic Acids Res. 12:9229-9236(1984).
CC -----
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CC -----
DR EMBL: X01668; -; NOT_ANNOTATED_CDS.
DR PIR: A01900; K3HUVG.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003506; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION VG.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 115 FRAMEWORK-4.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
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SQ SEQUENCE 115 AA: 12575 MW: 2DE47CDA3A17D555 CRC64:
Query Match
Best Local Similarity 100.0%; Score 43; DB 1; Length 115;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
Db 89 TDFTLTSS 97

RESULT 11
KV40_HUMAN STANDARD; PRT; 116 AA.
ID P04434;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region VH precursor (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85087932; PubMed=6440122;
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RL within the VK locus."
CC Nucleic Acids Res. 12:9229-9236(1984).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X02725; -; NOT_ANNOTATED_CDS.
DR PIR: A01901; K3HUVH.
DR HSSP: P01789; 2MCP.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_v.
DR SMART: SM00406; Ig_v.
DR Immunoglobulin V region; Signal.
KM SIGNAL 1 20
FT CHAIN 1 >116 IG KAPPA CHAIN V-III REGION VH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 77 FRAMEWORK-2.
FT DOMAIN 71 77 FRAMEWORK-3.
FT DOMAIN 78 109 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 116
SQ SEQUENCE 116 AA: 12757 MW: 51CDS5BA53B21929 CRC64:

Query Match
Best Local Similarity 100.0%; Score 43; DB 1; Length 116;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
Db 90 TDFTLTSS 98

RESULT 12
KV11_HUMAN STANDARD; PRT; 117 AA.
ID P06312;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
AC P01601;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region HK101 precursor (Fragment).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81098966; PubMed=6779204;
RA Bentley D.L., Rabbits T.H.;
RT "Human immunoglobulin variable region genes -- DNA sequences of two V
RL kappa genes and a pseudogene."
RL Nature 288:730-733(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83129397; PubMed=6402305;
RA Bentley D.L., Rabbits T.H.;
RT "Evolution of immunoglobulin V genes: evidence indicating that
RT recently duplicated human V kappa sequences have diverged by gene
RT conversion."
RL Cell 32:181-189(1983).
CC -----
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CC -----
CC EMBL: K01322; AAA58930.1; -
DR EMBL: K01324; AAA58932.1; -
DR EMBL: V00558; CA23824.1; -
DR PIR: A01881; K1H011.
DR PIR: A21056; A21056.
DR HSSP: P01607; 1REI.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_v.
DR SMART: SM00406; Ig_v.
DR Immunoglobulin V region; Signal.
KM SIGNAL 1 22
FT CHAIN 1 >117 IG KAPPA CHAIN V-I REGION HK101.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 FRAMEWORK-3.
FT DOMAIN 79 110 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 111 >117 FRAMEWORK-3.
FT DISULFID 45 110 COMPLEMENTARITY-DETERMINING-3.
FT NON_TER 117
SQ SEQUENCE 117 AA: 12799 MW: D7D0FF3718CF587 CRC64:

Query Match
Best Local Similarity 100.0%; Score 43; DB 1; Length 117;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
Db 91 TDFTLTSS 99

RESULT 13
KV40_HUMAN STANDARD; PRT; 121 AA.
ID P06312;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
```

```

DE Ig kappa chain V-IV region precursor (Fragment).
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G.; Bornkamm G.W.; Combiato G.; Mocikat R.; Pohlentz H.D.;
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene."
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -1- MISCELLANEOUS: THERE IS ONLY ONE IG KAPPA V-IV GENE.
CC -----
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CC -----
CC EMBL: Z00023; CAA77318.1; -.
DR PIR: A01802; KAHU.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; IgV_1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >121 IG KAPPA CHAIN V-IV REGION.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13380 MW; 9586AD418BD3974 CRC64;

Query Match 100.0%; Score 43; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFLTITSS 9
DB 95 TDFLTITSS 103

RESULT 14
KV1W_HUMAN STANDARD; PRT; 129 AA.
ID KV1W_HUMAN
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G.; Combiato G.; Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related."
RL Nucleic Acids Res. 12:6995-7006(1984).

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X00965; CAA25477.1; ALT_TERM.
DR PIR: A01883; KIHUWK.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; IgV_1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07DAFCA3F9 CRC64;

Query Match 100.0%; Score 43; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFLTITSS 9
DB 91 TDFLTITSS 99

RESULT 15
KV4B_HUMAN STANDARD; PRT; 133 AA.
ID KV4B_HUMAN
AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G.; Bornkamm G.W.; Combiato G.; Mocikat R.; Pohlentz H.D.;
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene."
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Z00022; CAA77317.1; -.
DR PIR: A01804; KAHUOI.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.

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DR Pfam: PF00047; Ig: 1.
 DR SMART: SMO0406; IGV: 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 133 IG KAPPA CHAIN V-IV REGION JI.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 61 75 FRAMEWORK-2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 83 114 FRAMEWORK-3.
 FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 123 132 FRAMEWORK-4.
 FT DISULFID 43 114 BY SIMILARITY.
 FT NON_TER 133
 SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match 100.0%; Score 43; DB 1; Length 133;
 Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TDFLTISS 9
 |||||
 Db 95 TDFLTISS 103

Search completed: July 15, 2002, 13:23:33
 Job time: 1449 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 13:22:46 ; Search time 172.49 seconds
(without alignments)
9.026 Million cell updates/sec

Title: US-09-712-819a-7
Perfect score: 43
Sequence: 1 TDFLTITSS 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL.19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	107	4 Q96SA9	Q96SA9 homo sapien
2	43	100.0	107	11 Q9ER29	Q9ER29 mus musculu
3	43	100.0	108	4 Q9UL77	Q9UL77 homo sapien
4	43	100.0	108	4 Q9UL70	Q9UL70 homo sapien
5	39	90.7	107	4 Q9UL81	Q9UL81 homo sapien
6	39	90.7	108	4 Q9UL83	Q9UL83 homo sapien
7	39	90.7	108	4 Q9UL79	Q9UL79 homo sapien
8	39	90.7	109	4 Q9UL86	Q9UL86 homo sapien
9	39	90.7	109	4 Q9UL85	Q9UL85 homo sapien
10	39	90.7	109	4 Q9UL78	Q9UL78 homo sapien
11	37	86.0	557	16 Q99XR2	Q99XR2 streptococ
12	36	83.7	99	11 Q9UL74	Q9UL74 mus musculu
13	35	81.4	116	4 Q96PF6	Q96PF6 homo sapien
14	35	81.4	1806	16 Q929J3	Q929J3 listeria in
15	34	79.1	284	12 Q9JGM1	Q9JGM1 kaposi's sa
16	33	76.7	104	11 Q9JL82	Q9JL82 mus musculu

17	33	76.7	114	4 Q9UL80	Q9UL80 homo sapien
18	33	76.7	233	11 Q91WS9	Q91WS9 mus musculu
19	33	76.7	234	11 Q91WF8	Q91WF8 mus musculu
20	33	76.7	238	11 Q99M37	Q99M37 mus musculu
21	33	76.7	269	5 Q00814	Q00814 tritrichomo
22	33	76.7	417	2 Q9RG03	Q9RG03 salmonella
23	33	76.7	520	16 Q9GM14	Q9GM14 pasteurella
24	33	76.7	572	10 Q9AT27	Q9AT27 phytophthor
25	33	76.7	640	5 Q9ELH9	Q9ELH9 samia cyth
26	33	76.7	927	16 Q9A579	Q9A579 caulobacter
27	33	76.7	4199	16 P74440	P74440 synechocyst
28	33	76.7	109	6 Q9N0M5	Q9N0M5 oryctolagus
29	32	74.4	127	11 Q92S59	Q92S59 mus musculu
30	32	74.4	319	1 Q9V2T0	Q9V2T0 pyrococcus
31	32	74.4	505	16 Q9KTE4	Q9KTE4 vibrio chol
32	32	74.4	573	4 Q9NM44	Q9NM44 homo sapien
33	32	74.4	583	4 Q9H587	Q9H587 homo sapien
34	32	74.4	596	2 Q9L7X7	Q9L7X7 bruceella ab
35	32	74.4	846	4 Q9H9J6	Q9H9J6 homo sapien
36	32	74.4	858	4 Q9H7W7	Q9H7W7 homo sapien
37	32	74.4	1450	5 Q26627	Q26627 strongyloce
38	32	74.4	1493	3 Q04002	Q04002 saccharomyc
39	32	74.4	1865	2 Q9XCJ1	Q9XCJ1 salmonella
40	31	72.1	102	16 Q91U11	Q91U11 pseudomonas
41	31	72.1	110	9 Q94MG5	Q94MG5 bacterioph
42	31	72.1	110	9 Q94MC3	Q94MC3 bacterioph
43	31	72.1	110	9 Q94MC2	Q94MC2 bacterioph
44	31	72.1	110	9 Q94MC1	Q94MC1 bacterioph
45	31	72.1	110	9 Q94MB9	Q94MB9 bacterioph

ALIGNMENTS

RESULT 1
ID Q96SA9 PRELIMINARY: PRT: 107 AA.
AC Q96SA9
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; Pubmed=9712075;
RA Aderson E.F., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -;
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4B843E9C5B577F16 CRC64;

Query Match 100.0%; Score 43; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.16; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 TDFLTITSS 9
Db 69 TDFLTITSS 77
RESULT 2
Q9ER29 PRELIMINARY: PRT: 107 AA.

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AC Q9ER29; 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
PT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Cloning and sequencing of the light chain fragment of variable region
RT genes of an anti-TNF- $\alpha$  monoclonal antibody."
RN J. Cell. Mol. Immunol. 12:21-26(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Construction and sequencing of the single-chain antibody gene of a
RT human TNF- $\alpha$  specific monoclonal antibody."
RN J. Cell. Mol. Immunol. 12:21-26(1996).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF262753; AAG23804.1; -
DR HSSP; P80362; 1WT.
DR InterPro; IPR003599; Ig_MHC.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00409; Ig_1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 107
FT SEQUENCE 107 AA; 11784 MW; 2B15E6A6604A26C3 CRC64;

Query Match 100.0%; Score 43; DB 11; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTSS 9
DB 72 TDFTLTSS 80

RESULT 3
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Pfam; PF00047; Ig_1.
RA SMART; SM00406; IGV; 1.

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FT NON_TER 1 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 100.0%; Score 43; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTSS 9
DB 69 TDFTLTSS 77

RESULT 4
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;

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Query Match 100.0%; Score 43; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFTLTSS 9
DB 69 TDFTLTSS 77

RESULT 5
Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-98277139; PubMed-9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;

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```
RT      "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL      fetus."
CLin. Immunol. Immunopathol. 87:184-192(1998).
DR      EMBL; AF035033; AAD56269.1; -.
DR      HSSP; P01607; 1RE1.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_V.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
FT      NON_TER 1
FT      NON_TER 107
SQ      SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match      90.7%; Score 39; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TDFTLTIS 8
Db      69 TDFTLTIS 76

RESULT 6
ID      Q9UL83      PRELIMINARY:      PRT; 108 AA.
AC      Q9UL83;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE      (FRAGMENT).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98277139; PubMed=9614934;
RA      Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA      Young D.C.;
RT      "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT      fetus."
RL      Clin. Immunol. Immunopathol. 87:184-192(1998).
DR      EMBL; AF035031; AAD56267.1; -.
DR      HSSP; P80362; 1WTL.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_V.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
FT      NON_TER 1
FT      NON_TER 108
SQ      SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EBA CRC64;

Query Match      90.7%; Score 39; DB 4; Length 108;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TDFTLTIS 9
Db      69 TDFTLTIS 77

RESULT 7
ID      Q9UL79      PRELIMINARY:      PRT; 108 AA.
AC      Q9UL79;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE      (FRAGMENT).
```

```
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98277139; PubMed=9614934;
RA      Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA      Young D.C.;
RT      "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT      fetus."
RL      Clin. Immunol. Immunopathol. 87:184-192(1998).
DR      EMBL; AF035035; AAD56271.1; -.
DR      HSSP; P01607; 1RE1.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_V.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
FT      NON_TER 1
FT      NON_TER 108
SQ      SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match      90.7%; Score 39; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TDFTLTIS 8
Db      69 TDFTLTIS 76

RESULT 8
ID      Q9UL86      PRELIMINARY:      PRT; 109 AA.
AC      Q9UL86;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      MYOSIN-REACTIVE IMMUNOGLOBULIN KAPPA CHAIN VARIABLE REGION
DE      (FRAGMENT).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98277139; PubMed=9614934;
RA      Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA      Young D.C.;
RT      "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT      fetus."
RL      Clin. Immunol. Immunopathol. 87:184-192(1998).
DR      EMBL; AF035028; AAD56264.1; -.
DR      HSSP; P80362; 1WTL.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_V.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
FT      NON_TER 1
FT      NON_TER 109
SQ      SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match      90.7%; Score 39; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TDFTLTIS 8
Db      70 TDFTLTIS 77
```

```
RESULT 9
Q9UL85 ID Q9UL85 PRELIMINARY: PRT: 109 AA.
AC Q9UL85:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN KAPPA CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035029; AAD56265.1; -.
DR HSSP; P80362; IWTU.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR003596; I9_V.
DR Pfam; PF00047; I9; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1 109
FT SEQUENCE 109 AA; 11646 MW; 5675C52EC7BE197 CRC64;

Query Match 90.7%; Score 39; DB 4; Length 109;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDEFTLTSS 9
Db 69 TDEFTLTSS 77

RESULT 10
Q9UL78 ID Q9UL78 PRELIMINARY: PRT: 109 AA.
AC Q9UL78:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035036; AAD56272.1; -.
DR HSSP; P80362; IWTU.
DR InterPro; IPR003006; I9_MHC.
DR InterPro; IPR003596; I9_V.
DR Pfam; PF00047; I9; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1 109
FT SEQUENCE 109 AA; 11646 MW; 5675C52EC7BE197 CRC64;
```

```
Query Match 90.7%; Score 39; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDEFTLTSS 8
Db 70 TDEFTLTSS 77

RESULT 11
Q99XR2 ID Q99XR2 PRELIMINARY: PRT: 557 AA.
AC Q99XR2:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE PUTATIVE FORMATE-TETRAHYDROFOLATE LIGASE (EC 6.3.4.3).
GN FHS.2 OR SPY2085.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Perrelli J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian X., Jia H.G., Najjar F.Z., Ken O., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT Complete genome sequence of an M1 strain of Streptococcus pyogenes.*;
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL; AE006628; AAK34738.1; -.
DR InterPro; IPR000559; FTHFS.
DR Pfam; PF01268; FTHFS; 1.
DR PROSITE; PS00722; FTHFS_2; 1.
KW ligase; Complete proteome.
FT SEQUENCE 557 AA; 59053 MW; CB07C9FCE90B34E7 CRC64;

Query Match 86.0%; Score 37; DB 16; Length 557;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDEFTLTSS 9
Db 505 TDEFTLTSS 513

RESULT 12
Q9JL74 ID Q9JL74 PRELIMINARY: PRT: 99 AA.
AC Q9JL74:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE ACT1-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BAIS/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206032; AAF69330.1; -.
DR HSSP; P80362; IWTU.
```


DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IgV_1.
 FT NON_TER 1
 FT NON_TER 99
 SQ SEQUENCE 99 AA; 10939 MW; 3B5D0E78453324 CRC64;

Query Match
 Best Local Similarity 83.7%; Score 36; DB 11; Length 99;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TDFLTITSS 9
 Db 61 TDFLTITSS 69

RESULT 13
 ID Q96PE6 PRELIMINARY; PRT; 116 AA.
 AC Q96PE6;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DE KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
 GN SDNK1
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RA MEDLINE-21361171; PubMed-11468171;
 RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
 RT "The tropism of organ involvement in primary systemic amyloidosis:
 RT contributions of Ig VL) germ line gene use and clonal plasma cell
 RT burden.";
 RL Blood 98:714-720(2001).
 DR EMBL; AF361758; AAK51465.1; -.
 FT NON_TER 1
 FT NON_TER 116
 FT NON_TER 116
 SQ SEQUENCE 116 AA; 12735 MW; E796FC217BRCF57 CRC64;

Query Match
 Best Local Similarity 81.4%; Score 35; DB 4; Length 116;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTITSS 9
 Db 69 TDFLTITSS 77

RESULT 14
 ID Q929J3 PRELIMINARY; PRT; 1806 AA.
 AC Q929J3;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DE PUTATIVE PEPTIDOLYCAN BOUND PROTEIN (LPXTG MOTIF).
 GN LINA282.
 OS Listeria innocua.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Listeria.
 OX NCBI_TaxID=1642;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIP 11262 / SEROVAR 6A;
 RX PubMed-11679669;
 RA Glaser P., Franjeul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,

RA Charbit A., Chetouani F., Couve E., de Daruvar A., Deloux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Krefl J., Kuhn M., Kunst F., Kutapat G.,
 RA Madueno E., Maloumnan A., Mata Vicente J., Ng E., Nedjati H.,
 RA Nordstiek G., Novella S., de Padlos B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schueller T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehlant J., Cossart P.;
 RT "Comparative genomics of *Listeria* species.";
 RL Science 294:849-852(2001).
 DR EMBL; AL596171; CAC97510.1; -.
 DR Listlist: LINA282; -.
 DR Hypothetical protein; Complete proteome.
 SQ SEQUENCE 1806 AA; 195670 MW; ABC808A65084972F CRC64;

Query Match
 Best Local Similarity 81.4%; Score 35; DB 16; Length 1806;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TDFLTITSS 9
 Db 372 TDFLTITSS 380

RESULT 15
 ID Q91GW1 PRELIMINARY; PRT; 284 AA.
 AC Q91GW1;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DE K1 GLYCOPROTEIN (FRAGMENT).
 GN K1.
 OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
 OC Vitruves; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Rhadinovirus.
 OX NCBI_TaxID=37296;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=UGD7;
 RA Kakoola D.N., Sheldon J., Dyabazaire M., Bowden R.J.,
 RA Katongole-Mbide E., Schulz T.F., Davison A.J.;
 RT "Recombination in human herpesvirus 8 strains from Uganda and
 RT evolution of the K15 gene.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY042942; AAK72676.1; -.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 284 AA; 31804 MW; BA224B08EDED38F CRC64;

Query Match
 Best Local Similarity 79.1%; Score 34; DB 12; Length 284;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TDFLTITSS 9
 Db 56 TDFLTITSS 64

Search completed: July 15, 2002, 13:22:47
 Job time: 1483 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 12:57:58 ; search time 228.39 seconds

(without alignments)
4.377 Million cell updates/sec

Title: US-09-712-819A-7

Perfect score: 43

Sequence: 1 TDFTLTSS 9

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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23: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	43	100.0	32	17 AAR87043	Human group I light
2	43	100.0	32	20 AAY52745	Humanised ATR-5 L
3	43	100.0	32	22 AAB98286	Anti-A33 antigen I
4	43	100.0	32	22 AAB98288	Anti-A33 antigen I
5	43	100.0	32	22 AAB97666	A33 antigen bindin
6	43	100.0	32	22 AAB97668	A33 antigen bindin
7	43	100.0	74	19 AAM62805	Amino acid sequenc
8	43	100.0	76	20 AAM62807	Variable kappa Ilg
9	43	100.0	82	19 AAM62807	Amino acid sequenc
10	43	100.0	84	17 AAM14491	Monoclonal antilbod
11	43	100.0	84	17 AAR99878	Monoclonal antilbod

12 43 100.0 86 19 AAM62806
13 43 100.0 88 19 AAM59619
14 43 100.0 88 21 AAY56654
15 43 100.0 88 21 AAY56655
16 43 100.0 88 21 AAY56657
17 43 100.0 88 21 AAY56659
18 43 100.0 94 19 AAM62808
19 43 100.0 94 22 AAB67510
20 43 100.0 95 16 AAR72061
21 43 100.0 95 16 AAR72062
22 43 100.0 95 16 AAR72063
23 43 100.0 95 16 AAR72064
24 43 100.0 95 16 AAR72065
25 43 100.0 95 16 AAR72058
26 43 100.0 95 16 AAR72059
27 43 100.0 95 16 AAR72060
28 43 100.0 101 20 AAY34316
29 43 100.0 102 21 AAY56683
30 43 100.0 103 22 AAG93599
31 43 100.0 104 15 AAR54318
32 43 100.0 104 17 AAM01285
33 43 100.0 104 21 AAM62803
34 43 100.0 104 21 AAY95137
35 43 100.0 104 21 AAY98246
36 43 100.0 105 15 AAR54310
37 43 100.0 105 17 AAR01268
38 43 100.0 105 17 AAR98495
39 43 100.0 105 17 AAR98497
40 43 100.0 105 17 AAR88717
41 43 100.0 105 19 AAM52243
42 43 100.0 105 19 AAM52231
43 43 100.0 105 19 AAM52237
44 43 100.0 105 19 AAM52239
45 43 100.0 105 19 AAM52241

ALIGNMENTS

RESULT 1
AAR87043
AAR87043 standard; Peptide; 32 AA.
AAR87043:
25-JUN-1996 (first entry)
Human group I light chain framework 3.
Humanised antibody; Interleukin-5; IL-5; recombinant antibody;
antibody engineering; monoclonal antibody; Mab; 39D10; CDR;
complementarity determining region; light chain; framework;
eosinophilia; allergy; asthma.
Homo sapiens.
W09535375-A1.
28-DEC-1995.
16-JUN-1995; 95WO-CB01411.
17-JUN-1994; 94GB-0012230.
(CULT) CELLTECH THERAPEUTICS LTD.
Athwal DS, Bodmer MW, Emlage JS;
WPI; 1996-058412/06.
Anti-human IL-5 recombinant antibody - useful for preventing or
reducing eosinophilia and for treating certain allergic diseases,
esp. asthma

XX Example 3; Fig 3; 69pp; English.
XX
XX Framework regions (AAR87041-44) of human group I (gpl) germ line
CC antibody light chain showed homology to corresponding regions
CC (AAR87045-48, respectively) of the rat anti-human interleukin-5
CC monoclonal antibody 39D10 light chain (see AAR87040). This homology
CC was utilized in the prodn. of a humanised 39D10 VL (AAR87057) in
CC which rat 39D10 VL complementarily determining regions were grafted
CC into the human gpl framework.
XX
SQ Sequence 32 AA:

Query Match 100.0%; Score 43; DB 17; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
Db 13 tdfLtlLSS 21

RESULT 2
AA52745
ID AAV52745 standard; Peptide: 32 AA.
XX
AC AAV52745;
XX
XX 26-JAN-2000 (first entry)
XX
XX Humanised ATR-5 L chain V region FR3 for "a".
XX
XX Human tissue factor; TF: humanised; antibody: mouse monoclonal antibody;
KW ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
KN disseminated intravascular coagulation; immunogenicity; chimeric.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN MO9951743-A1.
XX
PD 14-OCT-1999.
XX
XX 02-APR-1999; 99MO-JP01768.
XX
PR 03-APR-1998; 98JP-0091850.
XX
PA (CHUGAI SEIYAKU KK.
XX
PI Sato K, Adachi H, Yabuta N;
XX
XX WPI: 1999-620204/53.
XX
XX Humanised antibody recognizing human tissue factor, used for treatment
PT of disseminated intravascular coagulation -
XX
XX Claim 17; Page 270; 291pp; Japanese.
XX
XX The present invention describes chimeric antibody (Ab) heavy (H) chains
CC containing the variable region of the H chain of a mouse monoclonal Ab
CC recognising human tissue factor (hrf) and the constant region of the H
CC chain of a human Ab. The variable region is one of six specified
CC sequences (which are the H chain variable regions from mouse monoclonal
CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L)
CC chains containing the variable region of the L chain of a mouse
CC monoclonal Ab recognising human tissue factor (hrf) and the constant
CC region of the L chain of a human Ab, the variable region being one of six
CC specified sequences (which are the L chain variable regions from mouse
CC monoclonal Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for
CC the treatment and prevention of thrombotic disease, especially of
CC disseminated intravascular coagulation (DIC). The humanised antibody has
CC the high hrf binding activity of the mouse monoclonal antibody but

CC greatly reduced immunogenicity. AA23001 to AA23091 and Y527007 to
CC AA52767 represent sequences used in the exemplification of the present
CC invention.
XX
XX
SQ Sequence 32 AA:

Query Match 100.0%; Score 43; DB 20; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLTSS 9
Db 13 tdfLtlLSS 21

RESULT 3
AAB98286
ID AAB98286 standard; Peptide: 32 AA.
XX
AC AAB98286;
XX
XX 20-AUG-2001 (first entry)
XX
XX Anti-A33 antigen immunoglobulin VL FR3 SEQ ID NO:92.
XX
XX Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
KW immunoglobulin; complementarily determining region; CDR; cancer;
KN cytostatic; anticancer; colon cancer; stomach cancer.
XX
XX Homo sapiens.
XX
XX MO200130393-A2.
XX
XX 03-MAY-2001.
XX
XX 20-OCT-2000; 2000MO-US29289.
XX
XX 22-OCT-1999; 99US-0425638.
XX
PR 04-APR-2000; 2000US-0543004.
XX
XX (LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (SCRI) SCRIPPS RES INST.
XX
PI Barbas CF, Rader C, Ritter G, Welt S, Old LJ;
XX
XX WPI: 2001-328613/34.
XX
XX Treating cancers, particularly of stomach and colon, that express A33
PT antigen by administering conjugate of anticancer agent with specific
XX immunoglobulin product -
XX
XX Claim 16; Page 40; 85pp; English.
XX
XX The present invention describes a method for treating cancers that
CC express the A33 antigen. The method comprises administering an
CC anticancer agent (I) conjugated to an immunoglobulin product (II) that
CC binds specifically to A33 and contains one or more of 13 specified
CC complementarily determining regions (CDRs), given in AAB98262 to
CC AAB98274. (I) has cytostatic activity. The method can be used for
CC treating colon and stomach cancers. (II), or the nucleic acid encoding
CC it, can be used directly, in unconjugated form, for immunotherapy of
CC cancer, and, when labeled, for detection or diagnosis of diseases
CC associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to
CC AAB98321 represent sequences used in the exemplification of the
XX present invention.
XX
SQ Sequence 32 AA:

Query Match 100.0%; Score 43; DB 22; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLRTSS 9
 |||||
 Db 13 tdfcltiss 21

RESULT 4
 AAB98288
 ID AAB98288 standard; Peptide: 32 AA.

XX AC AAB98288;
 XX DT 20-AUG-2001 (first entry)
 XX DE Anti-A33 antigen immunoglobulin VL FR3 SEQ ID NO:94.

XX DE Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
 KW Immunoglobulin; complementarity determining region; CDR; cancer;
 KW cytosolic; anticancer; colon cancer; stomach cancer.

XX OS Homo sapiens.
 XX PN WO200130393-A2.

XX PD 03-MAY-2001.

XX PF 20-OCT-2000; 2000WO-US29289.

XX PR 22-OCT-1999; 99US-0425638.

XX PR 04-APR-2000; 2000US-0543004.

XX PA (LUDW-) LUDWIG INST CANCER RES.
 XX PA (SLOK) SLOAN KETTERING INST CANCER RES.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Barbas CF, Rader C, Ritter G, Welt S, Old LJ;

XX DR WPI; 2001-328613/34.

XX PT Treating cancers, particularly of stomach and colon, that express A33
 PT antigen by administering conjugate of anticancer agent with specific
 XX immunoglobulin product -
 XX PS Claim 16; Page 40; 85pp; English.

XX CC The present invention describes a method for treating cancers that
 CC express the A33 antigen. The method comprises administering an
 CC anticancer agent (I) conjugated to an immunoglobulin product (II) that
 CC binds specifically to A33 and contains one or more of 13 specified
 CC complementarity determining regions (CDRs), given in AAB98282 to
 CC AAB98774. (I) has cytosolic activity. The method can be used for
 CC treating colon and stomach cancers. (II), or the nucleic acid encoding
 CC it, can be used directly, in unconjugated form, for immunotherapy of
 CC cancer, and, when labeled, for detection or diagnosis of diseases
 CC associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to
 CC AAB98321 represent sequences used in the exemplification of the
 CC present invention.

XX SQ Sequence 32 AA;

Query Match 100.0%; Score 43; DB 22; Length 32;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLRTSS 9
 |||||
 Db 13 tdfcltiss 21

RESULT 5
 AAB97666

ID AAB97666 standard; Peptide: 32 AA.

XX AC AAB97666;

XX DT 08-AUG-2001 (first entry)

XX DE A33 antigen binding immunoglobulin product VLFR3 peptide SEQ ID NO:92.

XX KW Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
 KW immunoreact; anti A33 antigen antibody; immunoglobulin.

XX OS Homo sapiens.

XX PN WO200131065-A1.

XX PD 03-MAY-2001.

XX PF 20-OCT-2000; 2000WO-US29026.

XX PR 22-OCT-1999; 99US-0425638.

XX PR 04-APR-2000; 2000US-0543004.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Barbas CF, Rader C;

XX DR WPI; 2001-328657/34.

XX PT Preparing humanized rabbit antibodies that specifically immunoreact
 PT with a particular antigen using display technology for expressing
 XX libraries of antibody domains and fine tuning variable domain regions -
 XX PS Example 9; Page 39; 62pp; English.

XX CC The present invention describes a method for preparing a humanised rabbit
 CC antibody that specifically immunoreacts with a particular antigen. The
 CC method comprises expressing a library of antibodies comprising one or
 CC more complementarity determining region (CDR) from the variable domain
 CC sequences that specifically immunoreact with the antigen grafted into
 CC framework regions from humans, and selecting the antibodies that react
 CC with the antigen. The method is useful for humanising non-human
 CC mammalian antibodies, which can be used for the treatment of a variety
 CC of diseases. The present sequence represents an A33 antigen binding
 CC immunoglobulin product VLFR3 peptide which is given in an example from
 CC the present invention.

XX SQ Sequence 32 AA;

Query Match 100.0%; Score 43; DB 22; Length 32;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFTLRTSS 9
 |||||
 Db 13 tdfcltiss 21

RESULT 6
 AAB97668
 ID AAB97668 standard; Peptide: 32 AA.

XX AC AAB97668;

XX DT 08-AUG-2001 (first entry)

XX DE A33 antigen binding immunoglobulin product VLFR3 peptide SEQ ID NO:94.

XX KW Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
 KW immunoreact; anti A33 antigen antibody; immunoglobulin.

XX OS Homo sapiens.

PN W0200131065-A1.
XX
XX 03-MAY-2001.
PD
XX 20-OCT-2000; 2000MO-US29026.
PF
XX 22-OCT-1999; 9905-0425638.
PR
XX 04-APR-2000; 200005-0543004.
PR
XX (SCRI) SCRIPPS RES INST.
PA
XX Barbas CF, Rader C;
XX WPI: 2001-328657/34.
DR
XX
XX Preparing humanized rabbit antibodies that specifically immunoreact
PT with a particular antigen using display technology for expressing
PT libraries of antibody domains and fine tuning variable domain regions -
XX
PS Example 9; Page 39; 62pp; English.
XX
XX The present invention describes a method for preparing a humanised rabbit
CC antibody that specifically immunoreacts with a particular antigen. The
CC method comprises expressing a library of antibodies comprising one or
CC more complementarily determining region (CDR) from the variable domain
CC sequences that specifically immunoreact with the antigen grafted into
CC framework regions from humans, and selecting the antibodies that react
CC with the antigen. The method is useful for humanising non-human
CC mammalian antibodies, which can be used for the treatment of a variety
CC of diseases. The present sequence represents an A33 antigen binding
CC immunoglobulin product VLFR3 peptide which is given in an example from
CC the present invention.
CC
XX Sequence 32 AA:
SQ
Query Match 100.0%; Score 43; DB 22; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TDFLTITSS 9
Db 13 tdflltiss 21
RESULT 7
AAW62805
ID AAW62805 standard; Peptide; 74 AA.
XX
XX AAW62805;
AC
XX 23-SEP-1998 (first entry)
DT
XX
XX Amino acid sequence of a human antibody fragment.
DE
XX
XX Human; immunoglobulin; Ig; transgenic; non-human mammal;
KW inactivated endogenous Ig locus; B-cell development;
KW human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
KW kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
KW production; antibody.
XX
XX Homo sapiens.
OS
XX
XX W09824893-A2.
PN
XX 11-JUN-1998.
PD
XX
XX 03-DEC-1997; 97MO-US23091.
PF
XX
XX 03-DEC-1996; 9605-0759620.
PR
XX
XX (ABGE-) ABGENIX INC.
PA
XX

PI Green L, Jakobovits A, Klapholz S, Kucherlapati R;
PI Mendez M;
XX
XX WPI: 1998-333314/29.
DR
XX
XX New transgenic non-human mammals - having an inactivated
PT immunoglobulin locus and a near complete human immunoglobulin locus,
PT used for production of human antibodies
XX
PS Disclosure; Page 77; 128pp; English.
XX
XX AAW62793-822 represent fragments of human antibodies produced by
CC transgenic Xenomice created using the method of the invention. The
CC specification describes a transgenic non-human mammal which has genome
CC modifications that comprise an inactivated endogenous immunoglobulin (Ig)
CC locus, so that the mammal does not display normal B-cell development. The
CC modified genome also has an inserted human heavy chain Ig locus in
CC germline configuration, the human heavy chain Ig locus comprising a human
CC micro constant region and regulatory and switch sequences, human J-H
CC genes, human D-H genes, and human V-H genes and an inserted human kappa
CC light chain Ig locus in germline configuration, the human kappa light
CC chain Ig locus comprising a human kappa constant region, J-kappa genes,
CC and V-kappa genes, where the number of V-H and V-kappa genes inserted
CC are selected to restore normal B-cell development in the mammal. The
CC transgenic animals have a near complete human Ig locus, including both a
CC human heavy chain locus and a human kappa light chain locus. They can
CC be used for the production of human antibodies when exposed to
CC particular antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha
CC the mice will produce antibodies to IL-8, EGFR or TNF- alpha
CC respectively.
CC
XX Sequence 74 AA:
SQ
Query Match 100.0%; Score 43; DB 19; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TDFLTITSS 9
Db 48 tdflltiss 56
RESULT 8
AAW80981
ID AAW80981 standard; Protein; 76 AA.
XX
XX AAW80981;
AC
XX 30-MAR-1999 (first entry)
DT
XX
XX Variable kappa light region 012 encoded amino acid.
DE
XX
XX Human; epidermal growth factor receptor; tumour; EGF;
KW transforming growth factor alpha; TGF-alpha.
XX
XX Homo sapiens.
OS
XX
XX W09850433-A2.
PN
XX 12-NOV-1998.
PD
XX
XX 05-MAY-1998; 98MO-US09160.
PF
XX
XX 05-MAY-1997; 97US-0851362.
PR
XX
XX (ABGE-) ABGENIX INC.
PA
XX Gallo M, Jakobovits A, Jia X, Yang X;
PI WPI: 1999-034712/03.
DR
XX
XX humanised antibodies against epidermal growth factor receptor, EGF-r
PT

PT - useful to treat solid tumours whilst inducing reduced immunogenic
PT or allergic effects compared to mouse or mouse-derived antibodies
XX
XX Example 3; Page 105; 143pp; English.
XX
CC The variable kappa light region 012 encoded amino acid was used in the
CC production of anti-epidermal growth factor receptor (EGF-r) antibodies.
CC The antibodies can be administered therapeutically to patients (human or
CC veterinary) to treat solid tumours. EGF-r is overexpressed on many human
CC solid tumour types, and the fully human antibodies (i.e. comprising and
CC inhibit both epidermal growth factor (EGF) and transforming growth factor
CC alpha (TGF-alpha) binding to EGF-r (known to lead to cellular
CC proliferation and tumour growth). They can prevent tumour cell growth
CC and, in combination with an antineoplastic agent, may eradicate
CC established tumours. The fully human antibodies can minimise the
CC immunogenic and allergic responses intrinsic to previous mouse/rat or
CC mouse/rat-derived antibodies.
XX
SQ Sequence 76 AA;

Query Match 100.0%; Score 43; DB 20; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
0Y 1 TDFLTJISS 9
|||||||
DB 50 tdflltiss 58

RESULT 9
AAW62807
ID AAW62807 standard; Peptide; 82 AA.
XX
XX AAW62807;
AC
XX
XX 23-SEP-1998 (first entry)
DT
XX
DE Amino acid sequence of a human antibody fragment.
XX
XX Human; Immunoglobulin; Ig; transgenic; non-human mammal;
XX inactivated endogenous Ig locus; B-cell development;
XX human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
XX kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
XX production; antibody.
XX
XX Homo sapiens.
OS
XX
XX WO9824893-A2.
PN
XX
XX 11-JUN-1998.
PD
XX
XX 03-DEC-1997; 97WO-US23091.
PF
XX
XX 03-DEC-1996; 96US-0759620.
PR
XX
XX (ABGE-) ABGENIX INC.
PA
XX
XX Green L, Jakobovits A, Klapholz S, Kucherlapati R;
PI
XX
XX Mendez M;
PI
XX
XX WPI; 1998-33314/29.
DR
XX
XX New transgenic non-human mammals - having an inactivated
PT immunoglobulin locus and a near complete human immunoglobulin locus,
PT used for production of human antibodies
XX
XX Disclosure: Page 78; 128pp; English.
XX
XX AAW62793-822 represent fragments of human antibodies produced by
CC transgenic xenomice, created using the method of the invention. The
CC specification describes a transgenic non-human mammal which has genome
CC modifications that comprise an inactivated endogenous immunoglobulin (Ig)

CC locus, so that the mammal does not display normal B-cell development. The
CC modified genome also has an inserted human heavy chain Ig locus in
CC germline configuration, the human heavy chain Ig locus comprising a human
CC micro constant region and regulatory and switch sequences, human J-H
CC genes, human D-H genes, and human V-H genes and an inserted human kappa
CC light chain Ig locus in germline configuration, the human kappa light
CC chain Ig locus comprising a human kappa constant region, J-kappa genes,
CC and V-kappa genes, where the number of V-H and V-kappa genes inserted
CC are selected to restore normal B-cell development in the mammal. The
CC transgenic animals have a near complete human Ig locus, including both a
CC human heavy chain locus and a human kappa light chain locus. They can
CC be used for the production of human antibodies when exposed to
CC particular antigens e.g. when exposed to human IL-8, EGF or TNF- alpha
CC the mice will produce antibodies to IL-8, EGF or TNF- alpha
CC respectively.
XX
SQ Sequence 82 AA;

Query Match 100.0%; Score 43; DB 19; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
0Y 1 TDFLTJISS 9
|||||||
DB 56 tdflltiss 64

RESULT 10
AAW14491
ID AAW14491 standard; Protein; 84 AA.
XX
XX AAW14491;
AC
XX
XX 28-JAN-1997 (first entry)
DT
XX
XX Monoclonal antibody D VK.
DE
XX
XX heavy; light chain; monoclonal antibody; antigen 3; marker; melanoma;
XX permanent human tumour cell line; tumour-associated antigen; epitope;
XX gastrointestinal tumour; pancreatic carcinoma; diagnostic; therapeutic;
XX antigen 11; vitrio cholera; neuraminidase-resistant; ganglioside GD2.
XX
XX Synthetic.
OS
XX
XX EP27436-A1.
PN
XX
XX 21-AUG-1996.
PD
XX
XX 21-MAR-1990; 90EP-0105322.
PF
XX
XX 24-MAR-1989; 89DE-3909799.
PR
XX
XX (BEHW) BEHRINGER AG.
PA
XX
XX Auerbach B, Bosslet K, Sedlacek H, Seemann G;
PI
XX
XX WPI; 1996-372836/38.
DR
XX
XX N-PSDB; AAT63508.
PI
XX
XX Monoclonal antibody to tumour-associated antigen - useful as
PT gastrointestinal tumour marker
PT
XX
XX Disclosure: Page 14; 19pp; German.
XX
XX AAW14490-91 are the heavy and light chains (respectively) of monoclonal
CC antibody (Mab) D. Mab D recognises vitrio cholera
CC neuraminidase-resistant epitope of ganglioside GD2, from a human melanoma
CC cell line. Mabs A, B and C (see AAW1484-89) are mentioned in the
CC specification, but are not part of the claims. Mabs A and B recognise
CC antigens 3 and 11 resp., of a permanent human tumour cell line. Mab C
CC also recognises an epitope of a tumour-associated antigen. These antigens
CC occur at high concns. in the serum of patients with gastrointestinal

CC tumours, e.g. pancreatic carcinoma, and are thus useful as tumour markers
 CC for diagnostic or therapeutic purposes.
 XX

SO Sequence 84 AA:

Query Match 100.0%; Score 43; DB 17; Length 84;
 Best Local Similarity 100.0%; Pred. No. 0.36; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFLTRISS 9
 47 tdftriss 55

RESULT 11

AAR9878 ID AAR9878 standard; Protein; 84 AA.

AC AAR9878;

DE 28-JAN-1997 (first entry)

XX Monoclonal antibody D VK.

KW Monoclonal antibody; Mab; epitope: tumour-associated antigen;

XX marker; antigen.

OS Synthetic.

PN EP727435-A1.

PD 21-AUG-1996.

XX 21-MAR-1990; 90EP-0105322.

PR 24-MAR-1989; 89DE-3909799.

PA (BEHW) BEHRINGWERKE AG.

PI Auerbach B, Bosslet K, Sedlacek H, Seemann G;

DR WPI: 1996-372835/38.

DR N-PSDB: AAT36666.

PT Monoclonal antibody to tumour-associated antigen - useful as

PT gastrointestinal tumour marker

PS Disclosure; Page 14; 19pp; German.

XX Mab C (AAT36659-T36660) is a monoclonal antibody that recognises an

CC epitope of a tumour-associated antigen occurring at high concn. in

CC the serum of patients with gastrointestinal tumours, e.g. pancreatic

CC carcinoma, and is thus useful as a tumour marker for diagnostic or

CC therapeutic purposes.

CC Mabs A, B and D are mentioned in the specification, but are not

CC part of the claims.

CC Mab A (AAT36661-T36662) recognises antigen 3 of permanent human

CC tumour cell line.

CC Mab B (AAT36663-T36664) recognises antigen 11 of permanent human

CC tumour cell line.

CC Mab D (AAT36665-T36666) recognises a Vibrio cholera neuraminidase-

CC resistant epitope of ganglioside GD2, from a human melanoma cell

CC line.

XX Sequence 84 AA:

OY 1 TDFLTRISS 9

DB 47 tdftriss 55

RESULT 12

AAW62806 ID AAW62806 standard; Peptide; 86 AA.

AC AAW62806;

DE 23-SEP-1998 (first entry)

XX Amino acid sequence of a human antibody fragment.

KW Human; immunoglobulin; Ig; transgenic; non-human mammal;

KW inactivated endogenous Ig locus; B-cell development;

KW human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;

KW kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;

KW production; antibody.

XX Homo sapiens.

PN WO9824893-A2.

PD 11-JUN-1998.

XX 03-DEC-1997; 97WO-0523091.

PR 03-DEC-1996; 96US-0759620.

PA (ABGE-) ABGENIX INC.

PI Green L, Jakobovits A, Klapholz S, Kucheralapati R;

DR WPI: 1998-333314/29.

XX New transgenic non-human mammals - having an inactivated

PT immunoglobulin locus and a near complete human immunoglobulin locus,

PT used for production of human antibodies

PS Disclosure; Page 78; 128pp; English.

XX AAW62793-822 represent fragments of human antibodies produced by

CC transgenic Xenomice, created using the method of the invention. The

CC specification describes a transgenic non-human mammal which has genome

CC modifications that comprise an inactivated endogenous immunoglobulin (Ig)

CC locus, so that the mammal does not display normal B-cell development. The

CC modified genome also has an inserted human heavy chain Ig locus in

CC germline configuration, the human heavy chain Ig locus comprising a human

CC micro constant region and regulatory and switch sequences, human J-H

CC genes, human D-H genes, and human V-H genes and an inserted human kappa

CC light chain Ig locus in germline configuration, the human kappa light

CC chain Ig locus comprising a human kappa constant region, J-kappa genes,

CC and V-kappa genes, where the number of V-H and V-kappa genes inserted

CC are selected to restore normal B-cell development in the mammal. The

CC transgenic animals have a near complete human Ig locus, including both a

CC human heavy chain locus and a human kappa light chain locus. They can

CC be used for the production of human antibodies when exposed to

CC particular antigens e.g. when exposed to human IL-8, EGF or TNF- alpha

CC the mice will produce antibodies to IL-8, EGF or TNF- alpha

CC respectively.

XX Sequence 86 AA:

OY 1 TDFLTRISS 9

DB 48 tdftriss 56

PF 28-APR-1999; 99WO-US09131.
XX
PR 28-APR-1998; 98US-0083367.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Taylor AH;
XX
DR WPI; 2000-023265/02.
DR N-P-SDB; AA239323.
XX
PT Antibodies containing donor complementarity determining regions and
PT non-human primate acceptor frameworks, having reduced immunogenicity in
PT humans -
XX
PS Claim 22; Page 71; 123pp; English.
XX
CC The invention provides an antibody (Ab) comprising donor CDRs
CC (complementarily determining regions) derived from a non-human antigen-
CC specific donor antibody, and an acceptor framework from a non-human
CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
CC specific donor antibody onto homologous Old World ape or monkey acceptor
CC frameworks. The Abs have reduced immunogenicity and are better tolerated
CC in humans (because of the close similarity between the human and primate
CC proteins), but retain the full antigen-binding affinity of the donor
CC antibody.
XX
SQ Sequence 88 AA;

Query Match 100.0%; Score 43; DB 21; Length 88;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TDFTLRTISS 9
IIIIIIIIII
db 69 tdflltllss 77

Search completed: July 15, 2002, 12:57:58
Job time: 414 sec

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OM protein - protein search, using sw model

Run on: July 15, 2002, 12:59:19 ; Search time 75.67 Seconds
(without alignments)
2.905 Million cell updates/sec

Title: US-09-712-819A-7
Perfect score: 43
Sequence: 1 TDFITLTISS 9

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 segs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Parents AA:
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5h.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCIOS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	25	5	PCT-US91-02942-42
2	43	100.0	32	2	US-08-470-139-13
3	43	100.0	32	4	US-08-569-147-40
4	43	100.0	32	4	US-09-347-061-13
5	43	100.0	32	4	US-09-425-638A-92
6	43	100.0	32	4	US-09-425-638A-94
7	43	100.0	32	4	US-09-543-004-92
8	43	100.0	32	4	US-09-543-004-94
9	43	100.0	50	5	PCT-US91-02942-9
10	43	100.0	64	2	US-08-765-179B-10
11	43	100.0	64	2	US-08-765-179B-14
12	43	100.0	70	3	US-08-554-840-9
13	43	100.0	76	4	US-08-851-362D-21
14	43	100.0	80	3	US-08-554-840-12
15	43	100.0	80	3	US-08-554-840-13
16	43	100.0	80	3	US-08-554-840-15
17	43	100.0	93	3	US-08-783-853A-35
18	43	100.0	96	3	US-08-466-368-6
19	43	100.0	103	4	US-09-240-274-42
20	43	100.0	104	1	US-08-276-852-106
21	43	100.0	104	1	US-08-899-575-106
22	43	100.0	104	1	US-08-899-575-106
23	43	100.0	104	5	PCT-US95-08743-106
24	43	100.0	105	1	US-08-276-852-89
25	43	100.0	105	1	US-08-899-575-89
26	43	100.0	105	1	US-08-899-575-89
27	43	100.0	105	5	PCT-US95-08743-89

28	43	100.0	106	1	US-08-276-852-83	Sequence 83, Appl
29	43	100.0	106	1	US-08-276-852-85	Sequence 85, Appl
30	43	100.0	106	1	US-08-899-575-83	Sequence 83, Appl
31	43	100.0	106	1	US-08-899-575-85	Sequence 85, Appl
32	43	100.0	106	1	US-08-899-575-83	Sequence 83, Appl
33	43	100.0	106	3	US-08-899-575-85	Sequence 85, Appl
34	43	100.0	106	3	US-08-397-411-8	Sequence 8, Appl
35	43	100.0	106	4	US-09-240-274-159	Sequence 159, App
36	43	100.0	106	4	US-09-240-274-165	Sequence 165, App
37	43	100.0	106	5	PCT-US95-08743-83	Sequence 83, Appl
38	43	100.0	106	5	PCT-US95-08743-85	Sequence 85, App
39	43	100.0	107	1	US-07-634-278-103	Sequence 103, App
40	43	100.0	107	1	US-08-477-728-103	Sequence 83, Appl
41	43	100.0	107	1	US-08-276-852-82	Sequence 82, Appl
42	43	100.0	107	1	US-08-276-852-84	Sequence 84, Appl
43	43	100.0	107	1	US-08-276-852-104	Sequence 104, App
44	43	100.0	107	1	US-08-276-852-105	Sequence 105, App
45	43	100.0	107	1	US-08-300-386A-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1
Sequence 42, Application PC/TUS9102942
GENERAL INFORMATION:
APPLICANT: ROTHLEIN, ROBERT
APPLICANT: ADAIR, JOHN R
TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSER: Sterne, Kessler, Goldstein & Fox
STREET: 1225 Connecticut Ave. NW Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02942
FILING DATE: 19910429
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9009549.8
FILING DATE: 27-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: FOX, SAM L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 1011.0586600
TELEPHONE: (202) 833-8716
TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US91-02942-42

Query Match 100.0%; Score 43; DB 5; Length 25;
Best local similarity 100.0%; Pred. No. 0.058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TDFITLTISS 9
|||||

Db 6 TDFLTISS 14

RESULT 2

US-08-470-139-13

Sequence 13, Application US/08470139

Patent No. 5998586

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies

NUMBER OF SEQUENCES: 28

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/470,139

FILING DATE: 06 JUNE-1995

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: TRUJILLO, DOREEN YATKO

REGISTRATION NUMBER: 35,719

REFERENCE/DOCKET NUMBER: CARP-0044

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-470-139-13

Query Match

Best Local Similarity 100.0%; Score 43; DB 2; Length 32;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTISS 9

Db 13 TDFLTISS 21

RESULT 3

US-08-569-147-40

Sequence 40, Application US/08569147

Patent No. 6180377

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: HUMANISED ANTIBODIES

NUMBER OF SEQUENCES: 95

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

ADDRESS: No. 6180377ris, LLP

STREET: One Liberty Place - 46th Floor

CITY: Philadelphia

STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/569,147

FILING DATE: 25-March-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: TRUJILLO, DOREEN YATKO

REGISTRATION NUMBER: 35,719

REFERENCE/DOCKET NUMBER: CARP-0047

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:

LENGTH: 32 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-569-147-40

Query Match

Best Local Similarity 100.0%; Score 43; DB 4; Length 32;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTISS 9

Db 13 TDFLTISS 21

RESULT 4

US-09-347-061-13

Sequence 13, Application US/09347061

Patent No. 6316227

GENERAL INFORMATION:

APPLICANT: Bodmer, Mark

APPLICANT: Achwal, Diljeet Singh

APPLICANT: Emstage, John Spencer

TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies

FILE REFERENCE: CARP-0071

CURRENT APPLICATION NUMBER: US/09/347,061

CURRENT FILING DATE: 1999-07-02

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin version 3.0

SEQ ID NO 13

LENGTH: 32

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Consensus

US-09-347-061-13

Query Match

Best Local Similarity 100.0%; Score 43; DB 4; Length 32;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTISS 9

Db 13 TDFLTISS 21

RESULT 5

US-09-425-638A-92

Sequence 92, Application US/09425638A

Patent No. 6342587

GENERAL INFORMATION:

APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt an

TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THE

FILE REFERENCE: LUD 5630

CURRENT APPLICATION NUMBER: US/09/425,638A

CURRENT FILING DATE: 1999-10-22

NUMBER OF SEQ ID NOS: 129

SEQ ID NO 92

LENGTH: 32

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

US-09-425-638A-92

Query Match 100.0%; Score 43; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFLTITSS 9
|||||
DB 13 TDFLTITSS 21

RESULT 6
US-09-425-638A-94
; Sequence 94, Application US/09425638A
; Patent No. 6342587
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Rittler, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/425,638A
; CURRENT FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 94
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-425-638A-94

Query Match 100.0%; Score 43; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFLTITSS 9
|||||
DB 13 TDFLTITSS 21

RESULT 7
US-09-543-004-92
; Sequence 92, Application US/09543004
; Patent No. 6346249
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Rittler, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 92
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-92

Query Match 100.0%; Score 43; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFLTITSS 9
|||||
DB 13 TDFLTITSS 21

RESULT 8
US-09-543-004-94
; Sequence 94, Application US/09543004

; Patent No. 6346249
; GENERAL INFORMATION:
; APPLICANT: Carlos F. Barbas III, Christoph Rader, Gerd Rittler, Sydney Welt and
; APPLICANT: Lloyd J. Old
; TITLE OF INVENTION: A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREOF
; FILE REFERENCE: LUD 5630.1
; CURRENT APPLICATION NUMBER: US/09/543,004
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: 09/425,638
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 94
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-94

Query Match 100.0%; Score 43; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFLTITSS 9
|||||
DB 13 TDFLTITSS 21

RESULT 9
PCT-US91-02942-9
; Sequence 9, Application PC/TUS9102942
; GENERAL INFORMATION:
; APPLICANT: ROTHLEIN, ROBERT
; APPLICANT: ADAIR, JOHN R
; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Ave. NW Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentia Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02942
; FILING DATE: 19910429
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9009549.8
; FILING DATE: 27-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM L
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 1011.0586600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US91-02942-9

Query Match 100.0%; Score 43; DB 5; Length 50;

Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTISS 9
DB 24 TDFLTISS 32

RESULT 10
US-08-765-1798-10
Sequence 10, Application US/087651798
Patent No. 5854027
GENERAL INFORMATION:
APPLICANT: STEIPE, Boris
APPLICANT: STEINBACHER, Stefan
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY
TITLE OF INVENTION: OF ANTIBODIES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKALDO, Marnelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,1798
FILING DATE: 14-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02626
FILING DATE: 06-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 25 115.7
FILING DATE: 15-JUL-1994
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-765-1798-10

Query Match 100.0%; Score 43; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTISS 9
DB 38 TDFLTISS 46

RESULT 11
US-08-765-1798-14
Sequence 14, Application US/087651798
Patent No. 5854027
GENERAL INFORMATION:
APPLICANT: STEIPE, Boris
APPLICANT: STEINBACHER, Stefan
TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY
TITLE OF INVENTION: OF ANTIBODIES
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKALDO, Marnelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington

STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,1798
FILING DATE: 14-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02626
FILING DATE: 06-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 25 115.7
FILING DATE: 15-JUL-1994
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 64 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-765-1798-14

Query Match 100.0%; Score 43; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TDFLTISS 9
DB 38 TDFLTISS 46

RESULT 12
US-08-554-840-9
Sequence 9, Application US/0854840
Patent No. 6001358
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabil
APPLICANT: PADIAN, Eduardo A.
APPLICANT: NEWMAN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22113-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-554-840-9

Query Match 100.0%; Score 43; DB 3; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFLTITSS 9
|||||
DB 51 TDFLTITSS 59

RESULT 13
US-08-851-362D-21
Sequence 21, Application US/08851362D
Patent No. 623583
GENERAL INFORMATION:
APPLICANT: Jakobovits, Aya
APPLICANT: Yang, Xiao-Dong
APPLICANT: Gallo, Michael
APPLICANT: Jia, Xiao-Chi
TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
FILE REFERENCE: Cell 4.20
CURRENT APPLICATION NUMBER: US/08/851,362D
CURRENT FILING DATE: 1997-05-05
NUMBER OF SEQ. ID NOS.: 49
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 21
LENGTH: 76
TYPE: PRT
ORGANISM: human
US-08-851-362D-21

Query Match 100.0%; Score 43; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFLTITSS 9
|||||
DB 50 TDFLTITSS 58

RESULT 14
US-08-554-840-12
Sequence 12, Application US/08554840
Patent No. 6001358
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabil
APPLICANT: PADIAN, Eduardo A.
APPLICANT: NEWMAN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO.: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-554-840-12

Query Match 100.0%; Score 43; DB 3; Length 80;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TDFLTITSS 9
|||||
DB 51 TDFLTITSS 59

RESULT 15
US-08-554-840-13
Sequence 13, Application US/08554840
Patent No. 6001358
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabil
APPLICANT: PADIAN, Eduardo A.
APPLICANT: NEWMAN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO.: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-554-840-13

Query Match 100.0%; Score 43; DB 3; Length 80;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TDFTLTSS 9
 |||||
 Db 51 TDFTLTSS 59

Search completed: July 15, 2002, 12:59:19
 Job time: 390 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 13:01:02 ; Search time 95.45 seconds
(without alignments)
11.074 Million cell updates/sec

Title: US-09-712-819A-8
Perfect score: 58
Sequence: 1 YGRKKRRQRRK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :
1: pirl:.*
2: pirl2:.*
3: pirl3:.*
4: pirl4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	89.7	86	1	TNLJND
2	49	84.5	71	2	T09384
3	49	84.5	72	1	TNLJH4
4	49	84.5	86	1	TNLJZR
5	49	84.5	86	2	A25700
6	49	84.5	86	2	S54381
7	49	84.5	86	2	S33982
8	49	84.5	86	2	UC5591
9	49	84.5	87	2	T01665
10	49	84.5	95	1	TNLJ12
11	49	84.5	101	1	E44001
12	49	84.5	101	2	T09446
13	43	74.1	250	2	D38095
14	43	74.1	268	2	C38095
15	43	74.1	269	2	A38095
16	43	74.1	269	2	B38095
17	43	74.1	272	2	A38900
18	43	74.1	279	2	JH0402
19	43	74.1	303	2	JH0401
20	43	74.1	366	2	S61796
21	43	74.1	525	2	T48824
22	43	74.1	1022	2	S49127
23	42	72.4	128	2	H70457
24	42	72.4	431	2	S48908
25	42	72.4	552	2	UC4030
26	42	72.4	587	2	E96702
27	41	70.7	371	2	B39625
28	41	70.7	397	2	A39655
29	41	70.7	399	2	A39625

30	41	70.7	793	2	JC5539	Smoothed protein
31	40	69.0	509	2	A96563	probable protein k
32	39	67.2	148	2	S04807	hypothetical prote
33	39	67.2	153	2	T10115	replication-associ
34	39	67.2	333	2	JC7713	ankyrin-repeat pro
35	39	67.2	411	1	OOCVP2	p1 polypeptide - m
36	39	67.2	643	2	S46723	arginine--tRNA lig
37	39	67.2	743	2	B84767	hypothetical prote
38	39	67.2	747	1	A57107	kinasin-related pr
39	39	67.2	826	2	D86458	hypothetical prote
40	38	65.5	144	2	S46716	hypothetical prote
41	38	65.5	261	2	T09075	hypothetical prote
42	38	65.5	478	1	DPHDM2	methionyl aminopep
43	38	65.5	480	2	A46702	methionyl aminopep
44	38	65.5	517	2	T49173	hypothetical prote
45	38	65.5	683	2	T00872	probable protein k

ALIGNMENTS

```
RESULT 1
TNLJND
trans-activating transcription regulator - human immunodeficiency virus type 1 (isola
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: J00071
R:Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe,
Gene 81, 275-284, 1989
A:Title: Nucleotide sequence of HIV1-MDK: a highly cytopathic strain of the human immu
A:Reference number: J00065; MUID:90034200
A:Accession: J00071
A:Molecule type: DNA
A:Residues: 1-86 <SP1>
A:Cross-references: GB:M27323; NID:g328154; PIDN:AAA44866.1; PID:g328155
C:Genetics:
A:Gene: tat
C:Superfamily: AIDS trans-activating transcription regulator
C:Keywords: AIDS; immunodeficiency; transcription

Query Match 89.7%; Score 52; DB 1; Length 86;
Best Local Similarity 81.8%; Pred. No. 0.15;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YGRKKRRQRRK 11
|||||||
Db 47 YGRKKRRQRRK 57

RESULT 2
T09384
trans-activating transcription regulator - human immunodeficiency virus type 1 (isola
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: T09384
R:Michael, N.L.; Chang, G.; d'Arcy, L.A.; Ehrenberg, P.K.; Mariani, R.; Busch, M.P.;
J. VIROL. 69, 4228-4236, 1995
A:Title: Defective accessory genes in a human immunodeficiency virus type 1-infected
A:Reference number: Z1654; MUID:95287475
A:Accession: T09384
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-71 <MC>
A:Cross-references: EMBL:U24451; NID:g829440; PIDN:AAA79576.1; PID:g829444
C:Genetics:
A:Gene: tat
C:Superfamily: AIDS trans-activating transcription regulator
C:Keywords: transcription
```


C:Keywords: AIDS; immunodeficiency

Query Match 84.5%; Score 49; DB 2; Length 86;
Best Local Similarity 72.7%; Pred. No. 0.45;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRROKK 11
|||||
DB 47 YGRRKRROKK 57

RESULT 8

JC3591

transactivator protein - human immunodeficiency virus type 1

N:Alternate names: tat protein

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 17-Mar-1999

C:Accession: J05591

R:Hoffmann, S.; Willbold, D.

Biochem. Biophys. Res. Commun. 235, 806-811, 1997

A:Title: A selection system to study protein-RNA interactions: Functional display of HIV

A:Reference number: J05591; MUID:97350867

A:Accession: J05591

A:Molecule type: protein

A:Residues: 1-86 <HO2>

C:Comment: This protein is a key regulatory protein in the viral replication cycle and b

F:22-31/Region: cysteine-rich

Query Match 84.5%; Score 49; DB 2; Length 86;
Best Local Similarity 72.7%; Pred. No. 0.45;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRROKK 11
|||||
DB 47 YGRRKRROKK 57

RESULT 9

T01665

tat protein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 21-Jul-2000

C:Accession: T01665

R:Alizon, M.; Main-Hobson, S.; Gluckman, J.C.; Sonigo, P.

Cell 46, 63-74, 1986

A:Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol

A:Reference number: 214389; MUID:86245056

A:Accession: T01665

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-87 <ALT>

A:Cross-references: EMBL:K03456; NID:960228; PIDN:CAA28015.1; PID:960233

C:Genetics: 72/2

A:Introns: 72/2

C:Superfamily: AIDS trans-activating transcription regulator

Query Match 84.5%; Score 49; DB 2; Length 87;
Best Local Similarity 72.7%; Pred. No. 0.46;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRROKK 11
|||||
DB 47 YGRRKRROKK 57

RESULT 10

TN112

trans-activating transcription regulator - human immunodeficiency virus type 1 (isolate

C:Species: human immunodeficiency virus type 1, HIV-1

A>Note: host Homo sapiens (man)

C>Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 02-Jul-1998

C:Accession: A04017

R:Arya, S.K.; Gallo, R.C.

Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986

A:Title: Three novel genes of human T-lymphotropic virus type III: Immune reactivity

A:Reference number: A94093; MUID:86177573

A:Accession: A04017

A:Molecule type: DNA

A:Residues: 1-95 <ARY>

C:Genetics:

A:Gene: tat

C:Superfamily: AIDS trans-activating transcription regulator

C:Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 84.5%; Score 49; DB 1; Length 95;
Best Local Similarity 72.7%; Pred. No. 0.49;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRROKK 11
|||||
DB 56 YGRRKRROKK 66

RESULT 11

E44001

trans-activating transcription regulator - human immunodeficiency virus type 1 (strai

N:Alternate names: tat protein

C:Species: human immunodeficiency virus type 1, HIV-1

A>Note: host Homo sapiens (man)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Jul-1998

C:Accession: E44001

R:Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.

J. Virol. 66, 6587-6600, 1992

A:Title: Complete nucleotide sequence, genome organization, and biological properties

A:Reference number: A44001; MUID:93021387

A:Accession: E44001

A:Molecule type: DNA

A:Residues: 1-101 <LIY>

A:Cross-references: GB:M93258

C:Genetics:

A:Gene: tat

A:Introns: 72/2

C:Superfamily: AIDS trans-activating transcription regulator

C:Keywords: AIDS; immunodeficiency; transcription regulation

Query Match 84.5%; Score 49; DB 1; Length 101;
Best Local Similarity 72.7%; Pred. No. 0.52;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRROKK 11
|||||
DB 47 YGRRKRROKK 57

RESULT 12

T09446

tat protein - human immunodeficiency virus type 1 (strain JRTL)

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-Aug-1999

C:Accession: T09446

R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namaz

submitted to the EMBL Data Library, July 1996

A:Reference number: 216673

A:Accession: T09446

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-101 <PAN>

A:Cross-references: EMBL:063632; NID:91465777; PID:91465783

C:Genetics:

A:Gene: tat

A: Introns: 72/2
C: Superfamily: AIDS trans-activating transcription regulator

Query Match 84.5%; Score 49; DB 2; Length 101;
Best Local Similarity 72.7%; Pred. No. 0.52;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRROKK 11
|||||
DB 47 YGRRKRRORR 57

RESULT 13

D38095
T-cell-specific transcription factor 1 splice form D - human
N: Alternate names: transcription factor TCF-1D
C: Species: Homo sapiens (man)
C: Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 24-Sep-1999
C: Accession: D38095; S61877; S61800
R: van de Watering, M.; Oosterwegel, M.; Holstege, F.; Dooyes, D.; Suikerbuijk, R.; Geurt
J. Biol. Chem. 267, 8530-8536, 1992
A: Title: The human T cell transcription factor-1 gene. Structure, localization, and prom
A: Reference number: A38095; MUID:92235082
C: Genetics:
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-250 <MAN>
R: Mayer, K.; Wolff, E.; Clevers, H.; Ballhausen, W.G.
A: Cross-references: GB:X63901
submitted to the EMBL Data Library, January 1995
A: Description: The human high mobility group (HMG)-box transcription factor TCF-1: novel
A: Reference number: S61877
A: Accession: S61877
A: Molecule type: mRNA
A: Residues: 1-250 <MAN>
A: Cross-references: EMBL:247361; NID:g619881; PIDN:CAA87439.1; PID:g619882
R: Mayer, K.; Wolff, E.; Clevers, H.; Ballhausen, W.G.
Biochim. Biophys. Acta 1263, 169-172, 1995
A: Title: The human high mobility group (HMG)-box transcription factor TCF-1: novel isofo
A: Reference number: S61796; MUID:95367594
A: Accession: S61800
A: Status: nucleic acid sequence not shown
A: Molecule type: mRNA
A: Residues: 244-250 <MAN>
A: Cross-references: EMBL:247361
C: Genetics:
A: Introns: 32/3; 68/1; 97/2; 137/2; 191/3; 227/3; 243/3
C: Superfamily: unassigned HMG box proteins; HMG box homology
C: Keywords: alternative splicing; DNA binding; transcription factor
F:151-226/Domain: HMG box homology <HMG1>

Query Match 74.1%; Score 43; DB 2; Length 250;
Best Local Similarity 63.6%; Pred. No. 9.7;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YGRRKRROKK 11
|||||
DB 227 YGRRKRRORR 237

RESULT 14

C38095
T-cell-specific transcription factor 1 splice form C - human
N: Alternate names: transcription factor TCF-1C
C: Species: Homo sapiens (man)
C: Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 24-Sep-1999
C: Accession: C38095; S13449; S65007
R: van de Watering, M.; Oosterwegel, M.; Holstege, F.; Dooyes, D.; Suikerbuijk, R.; Geurt
J. Biol. Chem. 267, 8530-8536, 1992
A: Title: The human T cell transcription factor-1 gene. Structure, localization, and prom
A: Reference number: A38095; MUID:92235082

A: Accession: C38095
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-268 <MAN>
A: Cross-references: GB:X63901
R: van de Watering, M.; Oosterwegel, M.; Dooyes, D.; Clevers, H.
EMBO J. 10, 123-132, 1991
A: Title: Identification and cloning of TCF-1, a T lymphocyte-specific transcription f
A: Reference number: S13449; MUID:91114695
A: Accession: S13449
A: Molecule type: mRNA
A: Residues: 1-268 <MAN>
A: Cross-references: EMBL:X59871; NID:g36789; PIDN:CAA42528.1; PID:g36780
A: Note: the authors describe an additional C-terminal exon of splice form C, which is
erences A38095 and S61796
R: Mayer, K.; Wolff, E.; Clevers, H.; Ballhausen, W.G.
Biochim. Biophys. Acta 1263, 169-172, 1995
A: Title: The human high mobility group (HMG)-box transcription factor TCF-1: novel is
A: Reference number: S61796; MUID:95367594
A: Accession: S65007
A: Status: not compared with conceptual translation
A: Molecule type: mRNA
A: Residues: 244-268 <MAN>
A: Note: only a part of the coding sequence is given
C: Genetics:
A: Introns: 32/3; 68/1; 97/2; 137/2; 191/3; 227/3 244/1
C: Superfamily: unassigned HMG box proteins; HMG box homology
C: Keywords: alternative splicing; DNA binding; transcription factor
F:151-226/Domain: HMG box homology <HMG1>

Query Match 74.1%; Score 43; DB 2; Length 268;
Best Local Similarity 63.6%; Pred. No. 10;
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YGRRKRROKK 11
|||||
DB 227 YGRRKRRORR 237

RESULT 15

C38095
T-cell-specific transcription factor 1 splice form A - human
N: Alternate names: transcription factor TCF-1A
C: Species: Homo sapiens (man)
C: Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 21-Jul-2000
C: Accession: A38095; S18643; S65005
R: van de Watering, M.; Oosterwegel, M.; Holstege, F.; Dooyes, D.; Suikerbuijk, R.; G
J. Biol. Chem. 267, 8530-8536, 1992
A: Title: The human T cell transcription factor-1 gene. Structure, localization, and p
A: Reference number: A38095; MUID:92235082
A: Accession: A38095
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-269 <MAN>
A: Cross-references: EMBL:X59869; NID:g36791; PIDN:CAA56795.1; PID:g6006565
A: Note: authors translated the codon GAT for residue 253 as Ser
R: van de Watering, M.; Oosterwegel, M.; Dooyes, D.; Clevers, H.
EMBO J. 10, 123-132, 1991
A: Title: Identification and cloning of TCF-1, a T lymphocyte-specific transcription f
A: Reference number: S13449; MUID:91114695
A: Accession: S16645
A: Molecule type: mRNA
A: Residues: 1-269 <MAN>
A: Cross-references: EMBL:X59869; NID:g36785; PIDN:CAA42526.1; PID:g36786
R: Mayer, K.; Wolff, E.; Clevers, H.; Ballhausen, W.G.
Biochim. Biophys. Acta 1263, 169-172, 1995
A: Title: The human high mobility group (HMG)-box transcription factor TCF-1: novel is
A: Reference number: S61796; MUID:95367594
A: Accession: S65005
A: Status: not compared with conceptual translation
A: Molecule type: mRNA
A: Residues: 244-269 <MAN>

C:Genetics:
 A:introns: 32/3; 68/1; 97/2; 137/2; 191/3; 227/3; 244/1
 C:Superfamily: unassigned HMG box proteins; HMG box homology
 C:keywords: alternative splicing; DNA binding; transcription factor
 F:151-228/Domain: HMG box homology <HMG1>

Query Match 74.1%; Score 43; DB 2; Length 269;
 Best Local Similarity 63.6%; Pred No. 10;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YGKKRRROKK 11
 ||:||||:|
 Db 227 YGKKRRRSREK 237

Search completed: July 15, 2002, 13:01:03
 Job time: 469 sec

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OM protein - protein search, using sw model

Run on: July 15, 2002, 13:23:33 ; Search time 44.9 Seconds
(without alignments)
9,486 Million cell updates/sec

Title: US-09-712-819A-8
Sequence: 1 YGRKKRRQKK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	89.7	86	TAT_HV1ND	P18804 human immun
2	49	84.5	58	TAT_HV1B5	P04612 human immun
3	49	84.5	86	TAT_HV112	P04326 human immun
4	49	84.5	86	TAT_HV1B1	P04606 human immun
5	49	84.5	86	TAT_HV1B2	P04610 human immun
6	49	84.5	86	TAT_HV1B2	P04608 human immun
7	49	84.5	86	TAT_HV1B2	P04607 human immun
8	49	84.5	86	TAT_HV1B2	P12506 human immun
9	49	84.5	86	TAT_HV1B2	P04609 human immun
10	49	84.5	87	TAT_HV1B2	P04613 human immun
11	49	84.5	101	TAT_HV1A2	P04614 human immun
12	49	84.5	101	TAT_HV1C4	P05907 human immun
13	49	84.5	101	TAT_HV1C4	P05907 human immun
14	49	84.5	101	TAT_HV1C4	P05907 human immun
15	49	84.5	101	TAT_HV1C4	P05907 human immun
16	49	84.5	101	TAT_HV1C4	P05907 human immun
17	49	84.5	101	TAT_HV1C4	P05907 human immun
18	49	84.5	101	TAT_HV1C4	P05907 human immun
19	49	84.5	101	TAT_HV1C4	P05907 human immun
20	49	84.5	101	TAT_HV1C4	P05907 human immun
21	49	84.5	101	TAT_HV1C4	P05907 human immun
22	49	84.5	101	TAT_HV1C4	P05907 human immun
23	49	84.5	101	TAT_HV1C4	P05907 human immun
24	49	84.5	101	TAT_HV1C4	P05907 human immun
25	49	84.5	101	TAT_HV1C4	P05907 human immun
26	49	84.5	101	TAT_HV1C4	P05907 human immun
27	49	84.5	101	TAT_HV1C4	P05907 human immun
28	49	84.5	101	TAT_HV1C4	P05907 human immun
29	49	84.5	101	TAT_HV1C4	P05907 human immun
30	49	84.5	101	TAT_HV1C4	P05907 human immun
31	49	84.5	101	TAT_HV1C4	P05907 human immun
32	49	84.5	101	TAT_HV1C4	P05907 human immun
33	49	84.5	101	TAT_HV1C4	P05907 human immun

34	39	67.2	148	1	Y18K_MSVS	P14989 maize strea
35	39	67.2	153	1	Y18K_MSVN	P14978 maize strea
36	39	67.2	643	1	SYRM_YEAST	P36714 saccharomyc
37	39	67.2	747	1	KE3B_HUMAN	O15066 homo sapien
38	39	67.2	747	1	KE3B_MOUSE	O61771 mus musculu
39	38	65.5	144	1	YHP5_YEAST	P38808 saccharomyc
40	38	65.5	478	1	AMP2_HUMAN	P50579 homo sapien
41	38	65.5	478	1	AMP2_MOUSE	O08663 mus musculu
42	38	65.5	478	1	AMP2_RAT	P38062 rattus norv
43	38	65.5	794	1	SMO_CHICK	O42224 gallus gall
44	38	65.5	999	1	MFD_HELPJ	O26066 heliobacte
45	38	65.5	1001	1	MFD_HELPJ	O92357 heliobacte

ALIGNMENTS

RESULT	ID	STANDARD	PRT	86 AA.
TAT_HV1ND	TAT_HV1ND	STANDARD	PRT	86 AA.
AC	P18804			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	TAT protein (Transactivating regulatory protein).			
GN	TAT.			
OC	Human immunodeficiency virus type 1 (NDK isolate) (HIV-1).			
OC	Viruses; Retrovird viruses; Retroviridae; Lentivirus.			
OX	NCBI_Taxid-11695;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-90034200; PubMed-2806917;			
RA	Spire B., Sire J., Zacher V., Rey F., Barre-Sinoussi F., Galibert F.,			
RA	Hampe A., Chermann J.C.,			
RT	Nucleotide sequence of HIV-1-NDK: a highly cytopathic strain of the			
RT	Gene 81:275-284(1989).			
CC	-1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE			
CC	-1- TRANSCRIPTION RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND			
CC	ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR			
CC	PROMOTER.			
CC	-1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.			
CC	-1- MISCELLANEOUS: NDK, ISOLATED FROM A ZAIRIAN PATIENT AFFECTED WITH			
CC	AIDS. AND IS A HIGHLY CYTOPATHOGENIC STRAIN.			
CC	-----			
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CC	-----			
DR	EMBL; M27323; AAA44866.1; .			
DR	PIR; J00071; TNLJND.			
DR	HIV; M27323; TAT\$NDK.			
DR	InterPro: IPR001831; HIV_Tat.			
DR	Pfam: PF00539; Tat. 1.			
DR	PRINTS: PR00055; HIVTATDOMAIN.			
KW	Transcription regulation; Activator; RNA-binding; Nuclear protein;			
KW	AIDS.			
SQ	SEQUENCE 86 AA; 9711 MW; 7DB9B64E0AF8B0F4 CRC64;			

Query Match 89.7%; Score 52; DB 1; Length 86;
Best Local Similarity 81.8%; Pred. No. 0.024;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRKKRRQKK 11
DB 47 YGRKKRRQRRK 57

```

RESULT 2
TAT_HV1B5
ID TAT_HV1B5 STANDARD; PRT: 58 AA.
AC P04612;
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment).
GN TAT.
OS Human immunodeficiency virus type 1 (BHS isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
NCBI_TaxID=11682;
OX NCBI_TaxID=11682;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=6511123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumelster K., Ivanoff L., Peteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Pappas T.S., Chirayeb J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RT Nature 313:277-284(1985).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC -----
DR EMBL: K02012; AAA44656.1; -
DR HIV: K02012; TATSHS.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
FT NON_TER 58
SQ SEQUENCE 58 AA: 6800 MW: E36C21BF8F813E3 CRC64;
Query Match 84.5%; Score 49; DB 1; Length 58;
Best Local Similarity 72.7%; Pred. NO. 0.05;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 YGRKKRRQRRK 11
DB 47 YGRKKRRQRRR 57

```

```

RT "Three novel genes of human T-lymphotropic virus type III: Immune
RT reactivity of their products with sera from acquired immune
RT deficiency syndrome patients.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2209-2213(1986).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC -----
DR EMBL: M11840; AAA44999.1; -
DR PIR: A04017; TNLJ12.
DR HIV: M11840; TATSPCV12.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 86 AA: 9758 MW: 4DD60941FBE9115 CRC64;
Query Match 84.5%; Score 49; DB 1; Length 86;
Best Local Similarity 72.7%; Pred. NO. 0.074;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 YGRKKRRQRRK 11
DB 47 YGRKKRRQRRR 57

```

```

RESULT 4
TAT_HV1B1
ID TAT_HV1B1 STANDARD; PRT: 86 AA.
AC P04606;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (BHI0 isolate) (HIV-1), and
OS Human immunodeficiency virus type 1 (BHX3 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
NCBI_TaxID=11678; 11707;
OX NCBI_TaxID=11678, 11707;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-ISOLATE BHI0;
RA MEDLINE=8511123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumelster K., Ivanoff L., Peteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Pappas T.S., Chirayeb J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RT Nature 313:277-284(1985).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-ISOLATE HBX3;
RA MEDLINE=8528248; PubMed=2988795;
RA Crowl R., Ganugly K., Gordon M., Conroy R., Schaber M., Kramer R.,
RA Shaw G.W., Wong-Staal F., Reddy E.P.;
RT "HTLV-III env gene products synthesized in E. coli are recognized by
RT antibodies present in the sera of AIDS patients.";
RT Cell 41:979-986(1985).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE

```


Query Match	84.58;	Score 49;	DB 1;	Length 86;
Best Local Similarity	72.78;	Pred. No. 0.074;		
Matches	8;	Conservative	3;	Mismatches 0;
				Indels 0;
				Gaps 0;
QY	1	YGRKKRRQRRK	11	
Db	47	YGRKKRRQRRR	57	

```

RESULT 5
ID      TAT_HV1BR      STANDARD:      PRT;      86 AA.
AC      P04610;
DT      13-AUG-1987 (Rel. 05, Created)
DT      13-AUG-1987 (Rel. 05, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      TAT protein (Transactivating regulatory protein).
GN      TAT.
OS      Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC      Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX      NCBI_TaxID=11686;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=85099333; PubMed=2981635;
RT      Wein-Hobson S., Sonigo P., Danos O., Cole S., Alizon M.;
RL      Nucleotide sequence of the AIDS virus, LAV-1;
RN      Cell 40:9-17(1985).
RN      [2]
RA      SEQUENCE FROM N.A. (CLONE PNL4-3).
RT      Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.;
RL      Submitted (JUN-1988) to the EMBL/GenBank/DBD databases.
CC      -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC      TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC      ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE ITR
CC      PROMOTER.
CC      -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC      -----
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```

	RESULT	6
TAT_HV1H2		
ID	TAT_HV1H2	
AC	P04508; 009778;	STANDARD;
DT	13-JUL-1987 (Rel. 05	Created)
DT	15-JUL-1989 (Rel. 38,	Last update)
DT	16-OCT-2001 (Rel. 40,	Last annoucement update)
DT	16-OCT-2001 (Rel. 40,	Last annoucement update)

RESULT	6			
TAT_HV1H2				
ID	TAT_HV1H2	STANDARD:	PRT:	86 AA.
AC	PO4608; 009778;			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-JUL-1999 (Rel. 38, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	TAT protein (Transactivating regulatory protein).			
GN	TAT.			
OS	Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).			
OC	Viruses; Retrofold viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11706;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=6729196; PubMed=3040055;			
RA	Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,			
RA	Gallo R.C., Wong-Staal F.;			
RT	"Complete nucleotide sequences of functional clones of the AIDS			
RL	virus.";			
RL	AIDS Res. Hum. Retroviruses 3:57-69(1987).			
RN	[2]			
RP	REVISIONS.			
RA	Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,			
RA	Gallo R.C., Wong-Staal F.;			
RL	Submitted (Apr.1997) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE			
CC	TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND			
CC	ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR			
CC	PROMOTER.			
CC	-1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: NUCLEAR; CYTOSOL.			
CC	-----			
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CC	-----			
CC	EMBL: K03455; AAC50256.1; -			
CC	EMBL: AF033819; ABC82591.1; -			
DR	HTV; K03455; TATSHX82.			
DR	InterPro: IPR001831; HTV_Tat.			
DR	RefSeq: PF000539; Tat; 1.			
DR	PRINTS; PR00055; HIVTATDOMAIN.			
DR	Transcription regulation; Activator; RNA-binding; Nuclear protein;			

KW AIDS.
SQ SEQUENCE 86 AA: 9837 MW: 4DDC56D979769115 CRC64:

Query Match
Best Local Similarity 72.7%; Pred. No. 0.074;
Matches 8: Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKKRQKK 11
Db 47 YGRRKKRQRRR 57

RESULT 7

TAT_HV1PV STANDARD: PRT: 86 AA.

AC P04607;
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
CX NCBI_TaxID=11683;
CC (1)

RP SEQUENCE FROM N.A.
RX MEDLINE=8511157; PubMed=2982104;
RA Muesling M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
RA Capon D.J.;
RT "Nucleic acid structure and expression of the human
RT AIDS/lymphadenopathy retrovirus.";
RL Nature 313:450-458(1985).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.

CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.

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CC EMBL; K02083; AAB59870.1;
DR EMBL; X01762; ; NOT_ANNOTATED_CDS.
DR HIV; K02083; TATSPV22.

DR InterPro: IPR001831; HIV_Tat.

DR Pfam: PF00539; Tat; 1.

DR PRINTS: PR00055; HIVTATDOMAIN.

DR Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.

SQ SEQUENCE 86 AA: 9794 MW: 4DD56415FAF9015 CRC64:

Query Match
Best Local Similarity 72.7%; Score 49; DB 1; Length 86;
Matches 8: Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKKRQKK 11
Db 47 YGRRKKRQRRR 57

RESULT 8

TAT_HV12Z STANDARD: PRT: 86 AA.

AC P12506;
DT 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.

OS Human immunodeficiency virus type 1 (22/CDC-234 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
CX NCBI_TaxID=11683;
CC (1)

RP SEQUENCE FROM N.A.
RA Theodore T., Buckler-White A.;
RL Submitted (NOV-1988) to the HIV data bank.

CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.

CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.

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DR EMBL; M22639; AAA45363.1; -;
DR HIV; M22639; TATSPV22Z.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
DR Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.

SQ SEQUENCE 86 AA: 9737 MW: 97561D72AFCFF19 CRC64:

Query Match
Best Local Similarity 72.7%; Score 49; DB 1; Length 86;
Matches 8: Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKKRQKK 11
Db 47 YGRRKKRQRRR 57

RESULT 9

TAT_HV126 STANDARD: PRT: 86 AA.

AC P04609;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (Zaire 6 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
CX NCBI_TaxID=11708;
CC (1)

RP SEQUENCE FROM N.A.
RX MEDLINE=87248097; PubMed=3036660;
RA Sriyanasan A., Anand R., Ranganathan P., Feorino P.,
RA Schochetman G., Curran J., Kalyanaraman V.S., Luciw P.A.,
RA Sanchez-Pescador R.;
RT "Molecular characterization of human immunodeficiency virus from
RT Zaire: nucleotide sequence analysis identifies conserved and variable
RT domains in the envelope gene.";
RL Gene 52:71-82(1987).

CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.

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DR EMBL: K03458; AAA5377.1; -
DR PIR: C26192; TMLJ2R.
DR HIV: K03458; TAT526.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 86 AA; 9736 MW; E1E0AD741PFP5AC CRC64;

Query Match 84.5%; Score 49; DB 1; Length 86;
Best Local Similarity 72.7%; Pred. No. 0.074;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YGKKRRQKK 11
Db 47 YGKKRRQRR 57

RESULT 10
ID TAT_HV1A STANDARD; PRT; 87 AA.
AC P04613;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (MOL isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11697;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=86245056; PubMed=2424612;
RA Alizon M., Main-Jobson S., Montagnier L., Sonigo P.;
RT Genetic variability of the AIDS virus: nucleotide sequence analysis
RT of two isolates from African patients.*;
RL Cell 46:63-74(1986).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC
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DR EMBL: X04415; CA28015.1; -
DR HIV: K03456; TAT5MAL.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 87 AA; 10036 MW; 3832412849D5B1CE CRC64;

Query Match 84.5%; Score 49; DB 1; Length 87;
Best Local Similarity 72.7%; Pred. No. 0.075;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YGKKRRQKK 11
Db 47 YGKKRRQRR 57

RESULT 11
ID TAT_HV1A2 STANDARD; PRT; 101 AA.
AC P04614;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11685;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85090453; PubMed=2578227;
RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
RA Stempfen M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
RA Levy J.A., Dina D., Lucivi P.A.;
RT "Nucleotide sequence and expression of an AIDS-associated retrovirus
RT (ARV-2).";
RL Science 227:484-492(1985).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC
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DR EMBL: K02007; AAB59879.1; -
DR HIV: K02007; TAT5SF2.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 101 AA; 11557 MW; 1762370A3BD641FD CRC64;

Query Match 84.5%; Score 49; DB 1; Length 101;
Best Local Similarity 72.7%; Pred. No. 0.087;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YGKKRRQKK 11
Db 47 YGKKRRQRR 57

RESULT 12
ID TAT_HV1C4 STANDARD; PRT; 101 AA.
AC P05907;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (transactivating regulatory protein).
GN TAT.

OS Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OK NCBI_TaxID=11687;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=87041461; PubMed=3490666;
RA Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A.,
RA Andersen P.R., Devare S.G.;
RT "Molecular cloning and primary nucleotide sequence analysis of a
RT distinct human immunodeficiency virus isolate reveal significant
RT divergence in its genome sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC -----
CC EMBL: M13137; AAA44309.1; -.
CC DR PIR: B25523; TMJH4.
CC DR HIV: M13137; TATSCD45.
CC DR InterPro: IPR001831; HIV_Tat.
CC DR Pfam: PF00539; Tat; 1.
CC DR PRINTS: PR00055; HIVTATDOMAIN.
CC KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
KW SEQUENCE 101 AA; 11594 MW; 817D915F3FB1C7FA CRC64;
SO

OY 1 YGRRKRORRKK 11
DB 47 YGRRKRORR 57

Query Match 84.5%; Score 49; DB 1; Length 101;
Best Local Similarity 72.7%; Pred. No. 0.087;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
TAT_HV1JR STANDARD; PRT; 101 AA.
ID TAT_HV1JR
AC P20879;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (JRCSE isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OK NCBI_TaxID=11688;
RN (1)
RP SEQUENCE FROM N.A.
RA Koyanagi S., Chen I.S.Y.;
RL Submitted (DEC-1988) to the HIV data bank.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC -----
CC EMBL: M17449; AAA44851.1; -.
CC DR HIV: M17449; TATSMN.
CC DR InterPro: IPR001831; HIV_Tat.
CC DR Pfam: PF00539; Tat; 1.
CC DR PRINTS: PR00055; HIVTATDOMAIN.
CC KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
KW SEQUENCE 101 AA; 11634 MW; 2DBC7A21486389FF CRC64;
SO

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CC -----
CC EMBL: M38429; -; NOT_ANNOTATED_CDS.
CC DR HIV: M38429; TATJRCSE.
CC DR InterPro: IPR001831; HIV_Tat.
CC DR Pfam: PF00539; Tat; 1.
CC DR PRINTS: PR00055; HIVTATDOMAIN.
CC KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
KW SEQUENCE 101 AA; 11508 MW; 3B6C8D8FF7E8D4FA CRC64;
SO

OY 1 YGRRKRORRKK 11
DB 47 YGRRKRORR 57

Query Match 84.5%; Score 49; DB 1; Length 101;
Best Local Similarity 72.7%; Pred. No. 0.087;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
TAT_HV1MN STANDARD; PRT; 101 AA.
ID TAT_HV1MN
AC P05905;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OK NCBI_TaxID=11696;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;
RA Gargio C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates."
RL Virology 164:531-536(1988).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -1- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
CC PATIENT IN 1984.
CC -----
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CC -----
CC EMBL: M17449; AAA44851.1; -.
CC DR HIV: M17449; TATSMN.
CC DR InterPro: IPR001831; HIV_Tat.
CC DR Pfam: PF00539; Tat; 1.
CC DR PRINTS: PR00055; HIVTATDOMAIN.
CC KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
KW SEQUENCE 101 AA; 11634 MW; 2DBC7A21486389FF CRC64;
SO

OY 1 YGKKRRROKK 11
 |||||||:::
 DB 47 YGKKRRRORR 57

RESULT 15

TAT_HV10Y STANDARD; PRT; 101 AA.
 ID TAT_HV10Y
 AC P20893;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE TAT protein (Transactivating regulatory protein).
 GN TAT.
 OS Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90148544; Pubmed=2559749;
 RA Huët T., Dazza M.C., Brun-Vezinet F., Roelants G.E., Main-Hobson S.;
 RT "A highly defective HIV-1 strain isolated from a healthy Gabonese
 RT individual presenting an atypical western blot."; AIDS 3:707-715(1989).
 RL
 CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
 CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
 CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
 CC PROMOTER.
 CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
 CC -1- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A
 CC HEALTHY GABONESE INDIVIDUAL.
 CC -1- MISCELLANEOUS: THE SINGLE C -> S SUBSTITUTION AT RESIDUE 22 OF THE
 CC OVI TAT PROTEIN RENDERS IT INACTIVE, BUT MAY NOT ACCOUNT FOR THE
 CC AVIRULENCE OF THE VIRUS.
 CC
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL: M26727, AAA83395.1; -.
 CC DR HIV: M26727; TATSVI.
 CC DR InterPro: IPR001831; HIV_Tat.
 CC DR Pfam: PF00539; Tat; 1.
 CC DR PRINTS: PR00055; HIVTATDOMAIN.
 CC KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
 CC AIDS.
 CC SQ SEQUENCE 101 AA; 11561 MW; 83ACAC36CC4C87AD CRC64;

Query Match 84.5%; Score 49; DB 1; Length 101;
 Best Local Similarity 72.7%; Pred. No. 0.087;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 OY 1 YGKKRRROKK 11
 |||||||:::
 DB 47 YGKKRRRORR 57

Search completed: July 15, 2002, 13:23:34
 Job time: 1450 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2002, 13:22:47 ; Search time 172.49 Seconds
(without alignments)
11.032 Million cell updates/sec

Title: US-09-712-819A-8
Perfect score: 58
Sequence: 1 YGRKKRRQKK 11

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	89.7	72	15	099AP9 human immun
2	52	89.7	72	15	099AP7 human immun
3	52	89.7	72	15	099AP6 human immun
4	52	89.7	72	15	099AP5 human immun
5	52	89.7	72	15	099AP3 human immun
6	52	89.7	72	15	099AP2 human immun
7	52	89.7	72	15	099AN9 human immun
8	52	89.7	72	15	099AN8 human immun
9	52	89.7	72	15	099AN7 human immun
10	52	89.7	72	15	086025 human immun
11	52	89.7	72	15	075573 human immun
12	52	89.7	72	15	075574 human immun
13	52	89.7	72	15	P90144 human immun
14	52	89.7	101	15	091P33 human immun
15	52	89.7	101	15	0902K3 human immun
16	49	84.5	65	15	075540 human immun

17	49	84.5	65	15	075544 human immun
18	49	84.5	71	15	091OM7 human immun
19	49	84.5	71	15	091OM6 human immun
20	49	84.5	71	15	091OM5 human immun
21	49	84.5	71	15	091OM4 human immun
22	49	84.5	71	15	091OM3 human immun
23	49	84.5	71	15	091OM2 human immun
24	49	84.5	71	15	091OM1 human immun
25	49	84.5	71	15	091OM0 human immun
26	49	84.5	71	15	091OL9 human immun
27	49	84.5	71	15	091OL8 human immun
28	49	84.5	71	15	091OL7 human immun
29	49	84.5	71	15	091OL6 human immun
30	49	84.5	71	15	091OL5 human immun
31	49	84.5	71	15	091OL4 human immun
32	49	84.5	71	15	091OL3 human immun
33	49	84.5	71	15	091OL2 human immun
34	49	84.5	71	15	091OL1 human immun
35	49	84.5	71	15	091OL0 human immun
36	49	84.5	71	15	091OK9 human immun
37	49	84.5	71	15	091OK8 human immun
38	49	84.5	71	15	091OK6 human immun
39	49	84.5	71	15	091OK5 human immun
40	49	84.5	71	15	091OK4 human immun
41	49	84.5	71	15	091OK3 human immun
42	49	84.5	71	15	091OK2 human immun
43	49	84.5	71	15	091OK1 human immun
44	49	84.5	71	15	091OK0 human immun
45	49	84.5	71	15	040224 human immun

ALIGNMENTS

RESULT 1
ID 099AP9 PRELIMINARY; PRT; 72 AA.
AC 099AP9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSCRIPTIVATING REGULATORY PROTEIN) (FRAGMENT).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PARO. MOTHER:
RX MEDLINE-21322025; PubMed-11429117;
RA Husain M., Hahn T., Yedavalli V.R.K., Ahmad N.;
RT "Characterization of HIV Type 1 tat Sequences Associated with
RT Perinatal Transmission.";
RT AIDS Res. Hum. Retroviruses 17:765-773(2001).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANSCRIPTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: AY007056; AAG32103.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
FT NON_TER 72
SQ SEQUENCE 72 AA: 8342 MW: 603G524B7D9F2A8F CRC64;

Query Match 89.7%; Score 52; DB 15; Length 72;
Best Local Similarity 81.8%; Pred. No. 0.032;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 YGRKKRRQKK 11
|||||||:::|

DB 47 YGRRKRRQRRK 57

RESULT 2

099AP7 PRELIMINARY; PRT; 72 AA.

AC 099AP7; MEDLINE-21322025; PubMed-11429117.

DT 01-JUN-2001 (TEMBLrel. 17, Created)

DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)

DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)

DE TAT PROTEIN (TRANSCRIPTIVATING REGULATORY PROTEIN) (FRAGMENT).

GN TAT.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PAIRD, MOTHER;

RX MEDLINE-21322025; PubMed-11429117.

RA Husain M., Hahn T., Yedavalli V.R.K., Ahmad N.;

RT "Characterization of HIV type 1 tat Sequences Associated with Perinatal Transmission.";

DE AIDS Res. Hum. Retroviruses 17:765-773(2001).

RL AIDS Res. Hum. Retroviruses 17:765-773(2001).

CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR PROMOTER (BY SIMILARITY).

CC EMBL; AY007058; AAG32105.1; -.

DR InterPro; IPR001831; HIV_Tat.

DR Pfam; PF00539; Tat; 1.

DR PRINTS; PR00055; HIVTATDOMAIN.

KW Activator; Nuclear protein; RNA-binding; Transcription regulation.

FT NON TER 72

SO SEQUENCE 72 AA; 8342 MW; 603C524B7D9F2A8F CRC64;

QY 1 YGRRKRRQRRK 11

DB 47 YGRRKRRQRRK 57

Query Match 89.7%; Score 52; DB 15; Length 72;

Best Local Similarity 81.8%; Pred. No. 0.032;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 3

099AP6 PRELIMINARY; PRT; 72 AA.

AC 099AP6; MEDLINE-21322025; PubMed-11429117.

DT 01-JUN-2001 (TEMBLrel. 17, Created)

DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)

DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)

DE TAT PROTEIN (TRANSCRIPTIVATING REGULATORY PROTEIN) (FRAGMENT).

GN TAT.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PAIRD, MOTHER;

RX MEDLINE-21322025; PubMed-11429117.

RA Husain M., Hahn T., Yedavalli V.R.K., Ahmad N.;

RT "Characterization of HIV type 1 tat Sequences Associated with Perinatal Transmission.";

DE AIDS Res. Hum. Retroviruses 17:765-773(2001).

RL AIDS Res. Hum. Retroviruses 17:765-773(2001).

CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR PROMOTER (BY SIMILARITY).

CC EMBL; AY007059; AAG32106.1; -.

DR InterPro; IPR001831; HIV_Tat.

DR Pfam; PF00539; Tat; 1.

DR PRINTS; PR00055; HIVTATDOMAIN.

DR PRINTS; PR00055; HIVTATDOMAIN.

KW Activator; Nuclear protein; RNA-binding; Transcription regulation.

FT NON TER 72

SO SEQUENCE 72 AA; 8342 MW; 603C524B7D9F2A8F CRC64;

QY 1 YGRRKRRQRRK 11

DB 47 YGRRKRRQRRK 57

Query Match 89.7%; Score 52; DB 15; Length 72;

Best Local Similarity 81.8%; Pred. No. 0.032;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 4

099AP5 PRELIMINARY; PRT; 72 AA.

AC 099AP5; MEDLINE-21322025; PubMed-11429117.

DT 01-JUN-2001 (TEMBLrel. 17, Created)

DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)

DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)

DE TAT PROTEIN (TRANSCRIPTIVATING REGULATORY PROTEIN) (FRAGMENT).

GN TAT.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PAIRD, MOTHER;

RX MEDLINE-21322025; PubMed-11429117.

RA Husain M., Hahn T., Yedavalli V.R.K., Ahmad N.;

RT "Characterization of HIV type 1 tat Sequences Associated with Perinatal Transmission.";

DE AIDS Res. Hum. Retroviruses 17:765-773(2001).

RL AIDS Res. Hum. Retroviruses 17:765-773(2001).

CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR PROMOTER (BY SIMILARITY).

CC EMBL; AY007060; AAG32107.1; -.

DR InterPro; IPR001831; HIV_Tat.

DR Pfam; PF00539; Tat; 1.

DR PRINTS; PR00055; HIVTATDOMAIN.

KW Activator; Nuclear protein; RNA-binding; Transcription regulation.

FT NON TER 72

SO SEQUENCE 72 AA; 8352 MW; 766EC9318D9F2A8F CRC64;

QY 1 YGRRKRRQRRK 11

DB 47 YGRRKRRQRRK 57

Query Match 89.7%; Score 52; DB 15; Length 72;

Best Local Similarity 81.8%; Pred. No. 0.032;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 5

099AP3 PRELIMINARY; PRT; 72 AA.

AC 099AP3; MEDLINE-21322025; PubMed-11429117.

DT 01-JUN-2001 (TEMBLrel. 17, Created)

DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)

DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)

DE TAT PROTEIN (TRANSCRIPTIVATING REGULATORY PROTEIN) (FRAGMENT).

GN TAT.

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PAIRD, MOTHER;

RX MEDLINE-21322025; PubMed-11429117.

RA Husain M., Hahn T., Yedavalli V.R.K., Ahmad N.;


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RT *Characterization of HIV Type 1 tat Sequences Associated with
RT Perinatal Transmission."
RL AIDS Res. Hum. Retroviruses 17:765-773(2001).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: AY007062; AAC32109.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat.1.
DR PRINTS: PR00055; HIVTATDOMAIN.
DR Activator: Nuclear protein; RNA-binding; Transcription regulation.
FT NON_TER 72
SQ SEQUENCE 72 AA: 8355 MW; EF6855B4D8FC481 CRC64;

Query Match
Best Local Similarity 89.7%; Score 52; DB 15; Length 72;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKKRRQKK 11
| | | | | | | | | | |
DB 47 YGKKRRQRRK 57

RESULT 6
099AP2 PRELIMINARY; PRT: 72 AA.
ID 099AP2
AC 099AP2
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE TAR PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).
GN TAR.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PAIRD, MOTHER;
RX MEDLINE-21322025; PubMed-11429117;
RA Husain M., Hahn T., Yedavalli V.R.K., Ahmad N.;
RT *Characterization of HIV Type 1 tat Sequences Associated with
RT Perinatal Transmission."
RL AIDS Res. Hum. Retroviruses 17:765-773(2001).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: AY007063; AAC32110.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat.1.
DR PRINTS: PR00055; HIVTATDOMAIN.
DR Activator: Nuclear protein; RNA-binding; Transcription regulation.
FT NON_TER 72
SQ SEQUENCE 72 AA: 8342 MW; 603C524B7D9F2A8F CRC64;

Query Match
Best Local Similarity 89.7%; Score 52; DB 15; Length 72;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKKRRQKK 11
| | | | | | | | | | |
DB 47 YGKKRRQRRK 57

RESULT 7
099AN9 PRELIMINARY; PRT: 72 AA.
ID 099AN9
AC 099AN9
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
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DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE TAR PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).
GN TAR.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PAIRD, MOTHER;
RX MEDLINE-21322025; PubMed-11429117;
RA Husain M., Hahn T., Yedavalli V.R.K., Ahmad N.;
RT *Characterization of HIV Type 1 tat Sequences Associated with
RT Perinatal Transmission."
RL AIDS Res. Hum. Retroviruses 17:765-773(2001).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: AY007066; AAC32113.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat.1.
DR PRINTS: PR00055; HIVTATDOMAIN.
DR Activator: Nuclear protein; RNA-binding; Transcription regulation.
FT NON_TER 72
SQ SEQUENCE 72 AA: 8340 MW; 767E273F7D9F2A8F CRC64;

Query Match
Best Local Similarity 89.7%; Score 52; DB 15; Length 72;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGKKRRQKK 11
| | | | | | | | | | |
DB 47 YGKKRRQRRK 57
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RESULT 8
099AN8 PRELIMINARY; PRT: 72 AA.
ID 099AN8
AC 099AN8
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE TAR PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).
GN TAR.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PAIRD, MOTHER;
RX MEDLINE-21322025; PubMed-11429117;
RA Husain M., Hahn T., Yedavalli V.R.K., Ahmad N.;
RT *Characterization of HIV Type 1 tat Sequences Associated with
RT Perinatal Transmission."
RL AIDS Res. Hum. Retroviruses 17:765-773(2001).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: AY007067; AAC32114.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat.1.
DR PRINTS: PR00055; HIVTATDOMAIN.
DR Activator: Nuclear protein; RNA-binding; Transcription regulation.
FT NON_TER 72
SQ SEQUENCE 72 AA: 8352 MW; 766EC9318D9F2A8F CRC64;

Query Match
Best Local Similarity 89.7%; Score 52; DB 15; Length 72;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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OY 1 YGRRKRRQKK 11
 DB 47 YGRRKRRQRRK 57

RESULT 9

099AN7 PRELIMINARY: PRT: 72 AA.

AC 099AN7; 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).
 GN TAT.

OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11676;

RN 11

RP SEQUENCE FROM N.A.

RC STRAIN=PAIRD, MOTHER;

RX MEDLINE=21322025; PubMed=11429117;

RA Hsain M., Hahn T., Yedavalli V.R.K., Ahmad N.;

RT "Characterization of HIV Type 1 tat Sequences Associated with

Perinatal Transmission";

RL AIDS Res. Hum. Retroviruses 17:765-773(2001).

CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE

TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND

ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR

PROMOTER (BY SIMILARITY).

CC EMBL: AY007068; AAG32115.1; -

DR InterPro: IPR001831; HIV_Tat.

DR Pfam: PF005539; Tat; 1.

DR PRINTS: PR00055; HIVTATDOMAIN.

KM Activator; Nuclear protein; RNA-binding; Transcription regulation.

FT NON_TER 72

SO SEQUENCE 72 AA; 8342 MW; 603C524B7D9F2A8F CRC64;

Query Match 89.7%; Score 52; DB 15; Length 72;

Best Local Similarity 81.8%; Pred. No. 0.032;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRRQKK 11

DB 47 YGRRKRRQRRK 57

RESULT 10

086025 PRELIMINARY: PRT: 72 AA.

AC 086025; 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).
 GN TAT.

OS Human immunodeficiency virus type 1.

OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11676;

RN 11

RP SEQUENCE FROM N.A.

RC MEDLINE=95032920; PubMed=7946099;

RA Sabin E., Pan L.Z., Cheng-Wayer C., Mayer A.;

*Comparison of in vivo plasma and peripheral blood mononuclear cell

HIV-1 quasi-species to short-term tissue culture isolates: an analysis

of tat and C2-V3 env regions.";

RL AIDS 8:901-909(1994).

CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE

TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND

ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR

PROMOTER (BY SIMILARITY).

CC EMBL: U01437; AAA57782.1; -

DR InterPro: IPR001831; HIV_Tat.

DR Pfam: PF005539; Tat; 1.
 DR PRINTS: PR00055; HIVTATDOMAIN.
 KM Activator; Nuclear protein; RNA-binding; Transcription regulation.
 FT NON_TER 72

SO SEQUENCE 72 AA; 8406 MW; 7598236FEFEDB737 CRC64;

Query Match 89.7%; Score 52; DB 15; Length 72;

Best Local Similarity 81.8%; Pred. No. 0.032;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRRQKK 11

DB 47 YGRRKRRQRRK 57

RESULT 11

075573 PRELIMINARY: PRT: 72 AA.

AC 075573; 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).
 GN TAT.

OS Human immunodeficiency virus type 1.

OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11676;

RN 11

RP SEQUENCE FROM N.A.

RC STRAIN=110;

RA Lorenzo E., Herrera R.J., Lai S., Fischl M.A., Hill M.D.;

"The Tat and C2-V3 Envelope Genes in the Molecular Epidemiology of

Human Immunodeficiency Virus-1.";

RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE

TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND

ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR

PROMOTER (BY SIMILARITY).

CC EMBL: U57281; AAB17841.1; -

DR InterPro: IPR001831; HIV_Tat.

DR Pfam: PF005539; Tat; 1.

DR PRINTS: PR00055; HIVTATDOMAIN.

KM Activator; Nuclear protein; RNA-binding; Transcription regulation.

FT NON_TER 72

SO SEQUENCE 72 AA; 8306 MW; D3E506D0E08DF2E CRC64;

Query Match 89.7%; Score 52; DB 15; Length 72;

Best Local Similarity 81.8%; Pred. No. 0.032;

Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRRQKK 11

DB 47 YGRRKRRQRRK 57

RESULT 12

075574 PRELIMINARY: PRT: 72 AA.

AC 075574; 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).
 GN TAT.

OS Human immunodeficiency virus type 1.

OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

OX NCBI_Taxid=11676;

RN 11

RP SEQUENCE FROM N.A.

RC STRAIN=110;

```

Query Match Similarity      89.7%;   Score 52;   DB 15;   Length 72;
Best local Similarity      81.8%;   Pred. No. 0.032;
Matches      9;   Conservative      2;   Mismatches      0;   Indels      0;   Gaps      0;

QY      1 YGRRKKRRKKK 11
          |||||:::|
Db      47 YGRRKKRRKKK 57

RESULT 14
Q9YP33      PRELIMINARY;      PRT,      101 AA.

```

Query Match	89.7%	Score 52	DB 15	Length 101
Best local similarity	81.8%	Pred. No. 0.045		
Matches	9	Conservative	0	Indels
		Mismatches	0	Gaps
QY	1 YGRRRRRQKK 11			
	:::1			
DB	47 YGRRRRRQRRK 57			

Search completed: July 15, 2002, 13:22:47
Job time: 1483 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: July 15, 2002, 12:57:58 ; Search time 228.39 Seconds
(without alignments)
5.350 Million cell updates/sec

Title: US-09-712-819a-8
Perfect score: 58
Sequence: 1 YGRRKRQKK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq.032802:*
1: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1980.DAT:*
2: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1981.DAT:*
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11: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1990.DAT:*
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19: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1998.DAT:*
20: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA1999.DAT:*
21: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/hold-geneseq/genesqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	89.7	11	22	AAU09906 Interleukin 17 (hi
2	52	89.7	86	11	AAU09303 Sequence deduced f
3	49	84.5	11	19	AAU50263 HIV-1 tat protein.
4	49	84.5	11	20	AAU25075 TAR transduction d
5	49	84.5	11	20	AAU05415 Tat peptide. Unid
6	49	84.5	11	21	AAU03932 TAR protein transd
7	49	84.5	11	21	AAU03961 Minimal eleven ami
8	49	84.5	11	21	AAU03988 Beta-catenin deriv
9	49	84.5	11	21	AAU03598 Peptide associated
10	49	84.5	11	21	AAU03413 HIV TAR transducti
11	49	84.5	11	21	AAU09907 HIV tat protein tr

12	49	84.5	11	21	AAU93542 Amino acid sequenc
13	49	84.5	11	21	AAU71015 Human immunodefici
14	49	84.5	11	22	AAU09932 Human immunodefici
15	49	84.5	11	22	AAU09812 HIV-1 tat protein
16	49	84.5	11	22	AAU3064 Protein transducti
17	49	84.5	11	22	AAU12891 Human immunodefici
18	49	84.5	11	22	AAU65673 HIV tat protein fr
19	49	84.5	11	22	AAU50221 HIV-1 tat protein
20	49	84.5	11	22	AAU12605 Human immunodefici
21	49	84.5	11	22	AAU12204 Membrane transport
22	49	84.5	11	22	AAU60006 Internalising pept
23	49	84.5	11	22	AAU82757 HIV TAR protein tr
24	49	84.5	11	22	AAU85847 HIV-1 tat protein
25	49	84.5	11	22	AAU04300 Human immunodefici
26	49	84.5	11	22	AAU05268 HIV immunodefici
27	49	84.5	11	22	AAU98683 HIV TAR peptide fr
28	49	84.5	11	22	AAU03418 Human immunodefici
29	49	84.5	11	22	AAU03730 Protein transducti
30	49	84.5	11	22	AAU03815 HIV tat protein tr
31	49	84.5	11	22	AAU02973 Protein transducti
32	49	84.5	11	22	AAU68376 Human Cdk1 kinase
33	49	84.5	11	22	AAU70458 Human G2 checkpoint
34	49	84.5	11	22	AAU67673 Transduction domain
35	49	84.5	11	22	AAU73305 HIV-1 TAR protein
36	49	84.5	11	22	AAU69170 HIV tat protein tr
37	49	84.5	11	22	AAU69548 HIV tat protein tr
38	49	84.5	11	22	AAU70481 HIV TAR protein tr
39	49	84.5	11	22	AAU71756 NTR3 derived pepti
40	49	84.5	11	22	AAU71757 HIV TAR protein tr
41	49	84.5	12	14	AAU44159 Anti-herpetic pept
42	49	84.5	12	15	AAU49557 Residues 47-58 HIV
43	49	84.5	12	18	AAU1210 HIV-TAR protein tr
44	49	84.5	12	18	AAU26450 Peptide of the inv
45	49	84.5	12	19	AAU76156 HIV Type I TAR pro

ALIGNMENTS

RESULT	1	
AAU09906	standard; Protein: 11 AA.	
ID	AAU09906;	
AC	AAU09906;	
DT	14-FEB-2002 (first entry)	
XX	Interleukin 17 (hIL-17) receptor like protein associated peptide #1.	
DE	Interleukin 17 (hIL-17) receptor like protein associated peptide #1.	
XX		
KW	Interleukin 17; hIL-17 receptor like protein; immunomodulatory;	
KW	anti-inflammatory; anti-diabetic; immunosuppressive; anti-microbial;	
KW	hepatic; anabolic; anorectic; anti-IL2/IL6; anti-IL12/IL18; anti-IL10/IL13;	
KW	anti-convulsant; anti-asthmatic; dermatological; renal; osteopathic;	
KW	vascular; cytostatic; anti-leukemic; anti-fertility; ophthalmological;	
KW	hepatitis; anorexia; cachexia; neuronal dysfunction; lung disease;	
KW	bone disease; vascular disorder; eye disorder; cancer; human.	
XX		
OS	Synthetic.	
XX		
PN	W0200168859-A2.	
XX		
PD	20-SEP-2001.	
XX		
PF	15-MAR-2001; 2001WO-US08678.	
XX		
PR	16-MAR-2000; 2000US-189816P.	
PR	28-NOV-2000; 2000US-0724460.	
XX		
PA	(AMGE-) AMGEN INC.	
XX		
PI	Jing S;	
XX		
DR	WPI; 2001-611392/70.	

XX	Nucleic acids encoding interleukin 17 receptor like polypeptides.
PT	useful for preventing, diagnosing and treating, e.g. leukemia, asthma,
PT	diabetes, psoriasis and glaucoma -
XX	
PS	disclosure; page 149; 158pp; English.
XX	
CC	The invention describes novel nucleic acids encoding interleukin (IL) 17
CC	receptor like polypeptides useful as vaccines and in gene therapy. These
CC	have immunomodulatory, anti-inflammatory, anti-diabetic, anti-microbial,
CC	immunosuppressive, hepatic, anabolic, anorectic, anti-alzheimer's, renal,
CC	anti-parkinsonian, anti-convulsant, anti-ashtmatic, dermatological,
CC	osteopathic, vascular, cytostatic, anti-leukaemic, anti-fertility and
CC	ophthalmological activities. The IL-17 receptor like nucleic acids and
CC	proteins may be used to prevent and treat diseases associated with
CC	inappropriate IL-17 receptor like polypeptide (IL17rlp) expression. These
CC	include, for example immune disorders (e.g. inflammation, diabetes and
CC	transplant rejection), infections (e.g. hepatitis and septicemia),
CC	weight disorders (e.g. anorexia, cachexia and obesity), neuronal
CC	dysfunction (e.g. Alzheimer's disease, Parkinson's disease and epilepsy),
CC	lung disorders (e.g. cystic fibrosis, asthma and emphysema), skin disease
CC	(e.g. eczema and psoriasis), kidney disease (e.g. glomerulonephritis),
CC	bone diseases (e.g. osteoporosis and hypercalcaemia), vascular disorders
CC	(e.g. stroke and atherosclerosis), cancers (e.g. leukemia, myeloma and
CC	breast cancer), reproductive disorders (e.g. infertility and
CC	miscarriage), eye disorders (e.g. glaucoma and retinal neuropathy). The
CC	DNA and its complements may also used as diagnostic probes to detect and
CC	quantitate the presence of similar nucleic acids in samples and identify
CC	patients needing restorative therapy. The IL17rlp may also be used as
CC	antigens in the production of antibodies against the proteins and in
CC	assays to identify modulators of expression and activity. The
CC	anti-IL17rlp antibodies and antagonists may also be used to down regulate
CC	expression and activity.
CC	Note: This artificial peptide sequence is given in the sequence listing
CC	but is not described in the specification.
XX	
SO	Sequence 11 AA:
OY	1 YGRRKKRQKKK 11
DB	1 ygrrkkrrqrrk 11
RESULT 2	
ID AAR09303	
AC AAR09303;	
AA09303 standard: protein; 86 AA.	
DT 27-FEB-1991 (first entry)	
DE Sequence deduced from rat gene of HIV 1-NDR.	
KW Human Immunodeficiency Virus; AIDS.	
OS HIV 1-NDR.	
XX	
FT Key	Location/Qualifiers
FT Region	1..72
FT Region	/label= tat ex2
FT Region	73..86
FT Region	/label= tat ex3
PX WO9013630-A.	
PD 15-NOV-1990.	
PE 02-MAY-1990; 90MO-FR00312.	

```

PR 03-MAY-1989; 89FR-0005914.
XX
XX (INRM ) INSERM INST NAT SANTE.
PA
PI Barre-Sinoussi F, Chermann JC, Devaux C, Rey F, Sire J;
PI Sple B;
XX
XX WPI: 1990-361470/48.
DR
DR N-PSDB; AAO06635.
XX
XX New HIV-NDK retrovirus and protein component - used in vaccines
PT against immuno-deficiency disorders and in raising MAb's for
PT retro-virus detection in vivo.
XX
XX Disclosure; Fig 2; 37pp; French.
XX
XX The HIV NDK virus was isolated from peripheral blood lymphocytes of
CC an AIDS patient. A genomic library was prep'd. from DNA extracted
CC from CEM cells infected with the virus. The library was screened
CC with a pPRT probe corresp. to a fragment from HIV 1. The virus is
CC more cytopathic than other strains and is not inhibited by OKT4.
CC It has been deposited as CCM I-837. The sequence can be used to
CC express proteins useful for diagnosing the presence of NDK and
CC related viruses and in vaccines against immunodeficiency diseases.
CC See also AAR09301-4.
XX
XX Sequence 86 AA;
SQ
Query Match 89.7%; Score 52; DB 11; Length 86;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 YGRKKRRQKK 11
| | | | | | | | | |
DB 47 YGRKKRRGRK 57
RESULT 3
AAW50263
ID AAW50263 standard; Protein; 11 AA.
AC AAW50263;
XX
XX 20-JUL-1998 (first entry)
XX
XX HIV-1 tat protein.
XX
XX Mouse; BH3 interacting domain death agonist; BID; BCL-2 family;
KW apoptosis; regulation; cell death; inflammation; cancer; arthritis;
KW autoimmune disease; viral infection; lymphoproliferative.
XX
XX Human immunodeficiency virus type 1.
OS
XX
XX W09809980-A1.
XX
XX 12-MAR-1998.
XX
XX 09-SEP-1997; 97MO-US15872.
XX
XX 09-SEP-1996; 96US-0706741.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Korsmeyer SJ;
XX
XX WPI; 1998-193546/17.
XX
XX BH3 interacting domain death agonist polypeptide - used for treating
PT decreased apoptotic conditions resulting from inflammation etc.
XX
XX Example 8; Page 85; 118pp; English.

```

XX The present sequence represents the HIV-1 tat protein which is used in
CC an example of the present invention which describes a BH3 interacting
CC domain death agonist (BID) truncated protein. The BID protein, the
CC DNA encoding it or antisense sequences can be used for preventing or
CC treating a decreased apoptotic state of a cell. The decreased apoptotic
CC state that is treated results from a disease such as cancer, viral
CC infections, lymphoproliferative conditions, arthritis, inflammation and
CC autoimmune diseases. Antibodies against the BID protein can be used for
CC detecting a BID polypeptide in a cell or population of cell. The nucleic
CC acid sequence and the BID protein can also be used for treating
CC immunodeficiency disease (including AIDS), senescence, neurodegenerative
CC disease, ischaemic and reperfusion cell death, infertility and
CC wound-healing. Primers derived from the nucleic acid encoding the BID
CC protein can be used for detecting/quantitating the protein and for
CC detecting alterations in the nucleic acid encoding the BID protein.
XX Sequence 11 AA:

Query Match 84.5%; Score 49; DB 19; Length 11;
Best Local Similarity 72.7%; Pred. NO. 0.12;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRRQKK 11
|||||
Db 1 ygrkrrrrrr 11

RESULT 4
AAV25075
ID AAV25075 standard; peptide: 11 AA.

AC AAV25075;

DT 24-AUG-1999 (first entry)

DE TAT transduction domain peptide motif.

XX Anti-pathogen; fusion protein; protein transduction domain; PTD; AZT;
KW cytotoxic domain; suppressor; infection; medicament; ddi; ddC; dAT; 3TC;
KW PTC; DAPD; 1592U89; CS92; acyclovir; ganciclovir; peniclovir; interferon;
KW apoptosis; virus; HIV; cytomegalovirus; CMV; herpes simplex virus; HSV-1;
KW hepatitis virus; Kaposi's sarcoma-associated herpes virus; KSHV;
KW herpes virus; yellow fever virus; flavivirus; rhinovirus; plasmoidal;
KW transduction efficiency; cytotoxin.

XX Unidentified.

OS

PN MO929721-A1.

PD 17-JUN-1999.

PE 10-DEC-1998; 98WO-US26358.

PF 20-APR-1998; 98US-0082402.

PR 10-DEC-1997; 97US-0069012.

PA (UNITW) UNITW WASHINGTON.

PI Dowdy SF;

DR WPI; 1999-394958/33.

PT New anti-pathogen systems, particularly for virus and plasmodium
infections

PS Claim 65; Page 34; 123pp; English.
XX This invention describes a novel anti-pathogen system (APS) comprising a
CC fusion protein constructed from a covalently linked protein transduction
CC domain (PTD) and a cytotoxic domain. The APS can be used for suppressing
CC a pathogen infection in a mammal. The method may further comprise

CC administering a medicament e.g. AZT, ddi, ddC, dAT, 3TC, PTC, DAPD,
CC 1592089, CS92, acyclovir, ganciclovir, peniclovir or an interferon. The
CC APS can also be administered to a mammal in the presence of a pathogen to
CC induce apoptosis in a predetermined population of cells. The products can
CC be used for treating mammals suffering from or susceptible to a viral
CC infection or a disease associated with a virus, e.g. HIV, cytomegalovirus
CC (CMV), herpes simplex virus, e.g. type 1 (HSV-1) hepatitis virus, type C
CC (HCV), Kaposi's sarcoma-associated herpes virus (KSHV or human herpes
CC virus 8), yellow fever virus, flavivirus or rhinovirus, or suffering from
CC or susceptible to plasmoidal infection or a disease associated with a
CC plasmoidal infection, e.g. P. falciparum, P. vivax, P. ovale, or
CC P. malariae. The APS exhibits high transduction efficiency and
CC specifically kills or injures cells infected by one or more pathogens.
CC Formation of the cytotoxin is minimized or eliminated in uninfected cells
CC and in infected cells that keep the pathogen inactive. The APS can be
CC specifically tailored to kill or injure cells infected by one or more
CC pathogen strains. This sequence represents a TAT transduction domain
XX peptide motif which is used in the method of the invention.

SQ Sequence 11 AA:

Query Match 84.5%; Score 49; DB 20; Length 11;
Best Local Similarity 72.7%; Pred. NO. 0.12;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRRQKK 11
|||||
Db 1 ygrkrrrrrr 11

RESULT 5

AAV05415
ID AAV05415 standard; peptide: 11 AA.

AC AAV05415;

DT 02-JUL-1999 (first entry)

DE Tat peptide.

XX BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;
KW apoptosis promoter; cancer cell; virus infected cell; inflammation;
KW autoantibody producing cell; cancer; lymphoproliferative condition;
KW arthritis; autoimmune disease; therapy.

XX Unidentified.

OS

PN MO916787-A1.

PD 08-APR-1999.

PE 22-SEP-1998; 98WO-US19765.

PF 07-OCT-1997; 97US-0946039.

PR 26-SEP-1997; 97US-0060133.

PA (UNITW) UNITW WASHINGTON.

PI Korsmeyer SJ;

DR WPI; 1999-255058/21.

PT Bcl homology domain 3 polypeptide
infections

PS Claim 7; Page 67; 104pp; English.
XX This sequence represents a Tat peptide.
CC The invention relates to a bcl homology domain 3 (BH3 domain),
CC derived from a proapoptotic member of the BCL-2 family. The
CC BH3 polypeptide can be used in a method for promoting apoptosis in a
CC target cell, especially where the cell is a cancer cell or a virus infected
CC cell or an autoantibody producing cell. The BH3 polypeptide can be used

CC In therapeutic compositions for treating disease including cancer, other
CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune
CC diseases, which may result from the down regulation of cell death
CC regulation.
CC
XX
SQ Sequence 11 AA;

Query Match 84.5%; Score 49; DB 20; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.12;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRRKRRQKK 11
|||||
Db 1 ygrfkrrrrr 11

RESULT 6

AAB03932
ID AAB03932 standard; peptide: 11 AA.

AC AAB03932;

DT 26-FEB-2001 (first entry)

DE TAT protein transduction domain (internalisation moiety).

KW Modulating agent; beta-catenin; hair loss; hair growth; skin;
KW exfoliation; Alzheimer's disease; gene transcription;

KW cell differentiation; hearing loss; inner ear; hyperacusis; tinnitus;
KW hair regeneration.

XX Human immunodeficiency virus (HIV).

XX WO200059939-A1.

XX 12-OCT-2000.

XX 04-APR-2000; 2000WO-US09174.

XX 05-APR-1999; 99US-0288373.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Byers S, Gour BJ;

XX WPI; 2000-679355/66.

PT Modulating agents for inhibiting degradation of cytoplasmic
PT beta-catenin, used for e.g. stimulating hair growth or reducing hair
PT loss, inhibiting development of Alzheimer's disease, comprise
PT internalization moiety and amino acid sequence
XX
XX Claim 4; Page 46; 49pp: English.

XX Modulating agents for inhibiting degradation of cytoplasmic
XX beta-catenin are described. The modulating agent comprises an
XX internalization moiety and one or more of an amino acid sequence
XX SYDS(PQ.4)GHS(PQ.4)G, or a peptide analogue or peptidomimetic of
XX the amino acid sequence. The modulating agents are useful for the
XX manufacture of a medicament for stimulating hair growth or reducing
XX hair loss, stimulating skin exfoliation, and inhibiting the
XX development of Alzheimer's disease. They may also be used to
XX increase the beta-catenin level in a cell, to stimulate activation
XX of gene transcription in a cell, and to stimulate hearing loss
XX differentiation. They may further be used to ameliorate hearing loss
XX resulting from a variety of inner ear disorders, such as hyperacusis
XX and tinnitus, through regeneration of hair cells of the inner ear.

XX Sequence 11 AA;

Query Match, 84.5%; Score 49; DB 21; Length 11;

Best Local Similarity 72.7%; Pred. No. 0.12;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRRKRRQKK 11
|||||
Db 1 ygrfkrrrrr 11

RESULT 7

AAB03961
ID AAB03961 standard; Peptide: 11 AA.

AC AAB03961;

DT 26-FEB-2001 (first entry)

DE Minimal eleven amino acids present in PTAT.

KW Chimeric protein; fusion protein; FUSE like inhibitor protein;
KW FLIP; Fas; TNF; apoptosis; caspase-8; ligand; T cell; thymocyte;
KW tumour specific antigen; immune response; therapy; prophylaxis;
KW diagnosis; HIV; human immunodeficiency syndrome; AIDS;
KW acquired immune deficiency syndrome.

XX Human immunodeficiency virus.

XX WO200059935-A1.

XX 12-OCT-2000.

XX 05-APR-2000; 2000WO-US09002.

XX 05-APR-1999; 99US-0127867.

XX 06-APR-1999; 99US-0128021.

XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.

XX (PAIN/) PAIN C. SCHMINICH A.

XX (ALGE/) ALGECIRAS-SCHMINICH A;

XX Paya C, Algeciras-schminich A;

XX WPI; 2000-664988/64.

PT Fusion polypeptide useful for inhibiting ligand-induced apoptosis,
PT comprises portion of anti-apoptotic polypeptide linked to a transport
PT group
XX
XX Disclosure; Page 30; 89pp: English.

XX A chimeric group or fusion peptide which comprises a portion of an
XX anti-apoptotic polypeptide which inhibits apoptosis of lymphocytes in
XX combination with a transport group is described. The transport group
XX is capable of transporting the chimeric group or fusion peptide
XX across the cell membrane. The anti-apoptotic polypeptide is FLICE-like
XX inhibitor protein (FLIP) which inhibits Fas and TNF mediated apoptosis
XX by inhibiting binding of Caspase-8 to the Fas receptor complex, thus
XX shutting off the downstream Fas signalling pathway. The chimeric group
XX and fusion peptide are useful for inhibiting ligand-induced apoptosis
XX by bringing them into contact with T cells. The chimeric group is
XX useful for expanding T cells in vitro e.g. T cells specific for
XX particular antigens such as tumour-specific antigen, for enhancing
XX immune response and to inhibit the apoptosis of chronically activated
XX T cells e.g. activated CD4⁺ T cells in HIV infected patients. The
XX chimeric group is also useful for therapeutic, prophylactic or
XX diagnosis of intracellular delivery of small molecules and
XX macromolecules such as anti-apoptotic polypeptides and nucleic
XX acids encoding such polypeptides. Two primers (AA54297, AA54298) were
XX used to amplify the FLIP cDNA for subcloning into the XhoI-NcoI
XX site of the pHR-TAT vector which contains the N-terminal protein
XX transduction domain from the human immunodeficiency virus tat
XX protein. Tat is a preferred transport moiety.

XX Sequence 11 AA;

Query Match 84.5%; Score 49; DB 21; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.12;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRRKRRQKK 11
| | | | | | | | | | | | | |
Db 1 ygrkkrrrrrr 11

RESULT 8

AAB27088
ID AAB27088 standard; Peptide; 11 AA.

AC AAB27088;

DT 15-FEB-2001 (first entry)

DE Beta-catenin derived internalisation motety SEQ ID NO: 75.

KW Beta-catenin; cadherin-mediated intercellular adhesion;
KW cell differentiation; modulating agent; hair loss; skin exfoliation;
KW internalisation motety; flanking sequence; transcription; hearing loss.

OS Human immunodeficiency virus.

PN MO200053632-A1.

PD 14-SEP-2000.

PE 07-MAR-2000; 2000WO-CA00222.

PR 09-MAR-1999; 99US-0265107.

PA (UYMC-) UNIV MCGILL.

PI Blaschuk OW, Gour BJ;

WP: 2000-594308/56.

PT Stimulating beta-catenin mediated gene expression, cellular
PT differentiation and hair growth, involves contacting cells with
PT modulating agent capable of inhibiting interaction between alpha and
PT beta catenin

PS Disclosure; Page 19; 77pp; English.

XX The present invention is concerned with methods of modulating the amount
CC of free beta-catenin in the cell, and methods of stimulating the
CC expression of genes involved in cellular differentiation, the
CC transcription of which is under the control of beta-catenin. The
CC peptides given in AAB27053-B27086, AAB27284-B27300 and AAB27330-B27351
CC can be used as modulating agents which interrupt the interaction between
CC alpha and beta catenin, causing increased levels of the latter and
CC stimulating the activation of beta-catenin mediated transcription. This
CC can be used to stimulate cell differentiation, which can then be used to
CC promote hair growth and skin exfoliation. This latter is particularly
CC useful in the improvement of photodamaged skin and to minimise wrinkles.
CC The modulating peptide can also be used to reduce hearing loss resulting
CC from inner ear disorders such as hyperacusis and tinnitus.

SO Sequence 11 AA;

Query Match

Best Local Similarity 84.5%; Score 49; DB 21; Length 11;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRRKRRQKK 11
| | | | | | | | | | | | | |
Db 1 ygrkkrrrrrr 11

RESULT 9

AAB35698
ID AAB35698 standard; Peptide; 11 AA.

AC AAB35698;

DT 16-FEB-2001 (first entry)

DE Peptide associated with modified beta-catenin expression #31.

KW Beta-catenin; cell differentiation; hair growth;
KW cancer; Alzheimer's disease.

OS Human immunodeficiency virus type 1.

PN MO200063246-A2.

PD 26-OCT-2000.

PE 21-APR-2000; 2000WO-US10753.

PR 21-APR-1999; 99US-0296089.

PA (ADHE-) ADHEREX TECHNOLOGIES INC.

PI Blaschuk OW, Byers S, Gour BJ;

WP: 2000-679589/66.

PT Use of modulating agent comprising internalization motety and a
PT peptide for modulating beta-catenin mediated gene transcription and
PT cell differentiation, for treating cancer, and for inhibiting
PT Alzheimer's disease

PS Claim 6; Page 26; 47pp; English.

XX The present invention relates to a method for modulating beta-catenin
CC mediated gene transcription in a cell. The method involves contacting
CC a cell with a modulating agent comprising an internalization motety
CC and a peptide comprising a sequence LXXLL or peptide analogue of LXXLL.
CC The method is useful for modulating beta-catenin mediated gene
CC transcription, cell differentiation, hair growth, and retinoid acid
CC activity, for treating cancer, and for inhibiting the development of
CC Alzheimer's disease.

SO Sequence 11 AA;

Query Match 84.5%; Score 49; DB 21; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.12;

Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRRKRRQKK 11
| | | | | | | | | | | | | |
Db 1 ygrkkrrrrrr 11

RESULT 10

AAB29413
ID AAB29413 standard; peptide; 11 AA.

AC AAB29413;

DT 09-FEB-2001 (first entry)

DE HIV TAR transduction domain, SEQ ID NO:2.

KW Protein transduction domain; fusion molecule; therapeutic agent;
KW drug targeting; drug discovery; cell transduction; bioavailability;
KW vaccine; nervous system disorder; Alzheimer's disease;
KW Parkinson's disease; Huntington's disease; pre-senile dementia; epilepsy;
KW seizure; compulsive behaviour; meningitis; encephalitis; ischaemia;

KM spongiform encephalopathy; dyslexia; age-related memory loss;
 KM Lou Gehrig's disease; viral infection; HIV; bacterial infection.
 OS Human immunodeficiency virus.
 XX
 XX
 XX WO200062067-A1.
 PN 19-OCT-2000.
 PD
 XX 28-FEB-2000; 2000WO-US05097.
 PF
 XX 28-FEB-1999; 99US-0122757.
 PR 29-AUG-1999; 99US-0151291.
 XX
 XX (UNIT) UNIV WASHINGTON.
 PA
 XX Dowdy SF;
 PI
 XX WPI; 2000-647439/62.
 DR
 XX
 XX Fusion molecules comprising protein transduction domains and
 PT therapeutic agents, useful for treating e.g. Alzheimer's and
 PT Parkinson's diseases, dementia and epilepsy -
 XX
 XX Disclosure; Page 50; 191pp; English.
 PS
 XX The invention relates to a novel fusion molecule comprising at least
 CC one protein transduction domain (PTD) and at least one linked molecule,
 CC where the linked molecule has therapeutic or prophylactic activity
 CC against a medical condition. The invention also relates to methods of
 CC drug discovery in which the test compound is linked to a suitable
 CC transducing protein and introduced to a cell; a method of killing
 CC resistant microorganisms using a suitable fusion molecule; a mammal
 CC comprising a covalently linked fusion molecule; and a mammal adapted for
 CC experimental use in which at least one transduction molecule has been
 CC transduced into essentially all the cells of the mammal. The fusion
 CC molecule is used to deliver a therapeutic agent to a mammal, especially
 CC a human. The linked molecule may be a vaccine, an anti-infective drug,
 CC a cardiovascular drug, an antitumour drug, an analgesic, an
 CC anti-inflammatory, a diagnostic marker or a drug for the treatment or
 CC prevention of a central or peripheral nervous system disorder. The
 CC central nervous system (CNS) disorder is especially Alzheimer's disease,
 CC Parkinson's disease, Huntington's disease, and also includes pre-senile
 CC dementia, epilepsy and seizures, compulsive behaviour, meningitis
 CC (including viral and bacterial meningitis), encephalitis, ischaemia,
 CC scrapie (or related spongiform encephalopathies), dyslexia, age-related
 CC memory loss or Lou Gehrig's disease. Fusion molecules can also be
 CC used to kill virally infected cells, especially those infected with HIV.
 CC The vaccines are used to treat or prevent bacterial or viral infections.
 CC The methods are a highly effective means for transducing a molecule
 CC into an entire mammal or into specific cells, tissues, organs and
 CC systems within it. They also overcome bioavailability problems that
 CC are associated with many therapeutic agents (e.g., large molecular size,
 CC hydrophobicity, hydrophilicity, biological resistance), by providing
 CC efficient transduction of the target cell. The present sequence
 CC represents a protein transduction domain used in the invention.
 CC
 XX
 XX Sequence 11 AA;
 SO

Query Match 84.5%; Score 49; DB 21; Length 11;
 Best Local Similarity 72.7%; Pred. No. 0.12;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRQKK 11
 |||||||
 DB 1 YGRRKRQRR 11

RESULT, 11
 AAB09907
 ID AAB09907 standard; peptide; 11 AA.
 XX

AC AAB09907;
 XX
 DT 06-NOV-2000 (first entry)
 XX
 XX HIV tat protein transduction domain.
 DE
 XX Targeting signal; MUC-1; immunosuppression; autoimmune disorder;
 KM immune disorder; inflammatory disorder.
 KM
 OS Human immunodeficiency virus.
 XX
 XX WO200034468-A2.
 PN 15-JUN-2000.
 PD
 XX 09-DEC-1999; 99WO-US29016.
 PF
 XX 11-DEC-1998; 98US-011973.
 PR
 XX (BIOM-) BIOMIRA INC.
 PA
 XX Agrawal B, Longenecker BM,
 PI
 XX WPI; 2000-423418/36.
 DR
 XX
 XX Use of agent capable of intracellularly inhibiting mucin MUC-1 for
 PT inducing T-cell based immunosuppression and for treating autoimmune
 PT disorders, transplant rejection and inflammatory disorders -
 XX
 XX Disclosure; Page 15; 51pp; English.
 PS
 XX The present sequence is the tat protein transduction domain from HIV,
 CC which can be used as a targeting signal. It can be used to internalise
 CC sequences, such as MUC-1 antagonists, within the cell. MUC-1 is a
 CC immunosuppressor, and antagonists act to reduce overactive immune
 CC responses. Thus, the peptide can be used to treat inflammatory disorders
 CC such as rheumatoid arthritis, psoriasis, allergic contact dermatitis and
 CC ankylosing spondylitis, autoimmune disorders including myasthenia gravis,
 CC systemic lupus erythematosus, polyarteritis nodosa, Goodpastures
 CC syndrome, isopathic thrombocytopenic purpura, pernicious anaemia,
 CC anaemia, Graves' disease, rheumatic fever, peritonsillar abscess,
 CC insulin-resistant diabetes mellitus, bullous pemphigoid, pemphigus
 CC vulgaris, viral myocarditis, autoimmune thyroiditis, male infertility,
 CC sarcoidosis, allergic encephalomyelitis, multiple sclerosis, Sjogrens
 CC disease, Reiter's disease, Celliac disease, sympathetic ophthalmia and
 CC primary biliary cirrhosis, immune disorders, graft versus host disease
 CC and transplant rejection.
 CC
 XX
 XX Sequence 11 AA;
 SO

Query Match 84.5%; Score 49; DB 21; Length 11;
 Best Local Similarity 72.7%; Pred. No. 0.12;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRKRQKK 11
 |||||||
 DB 1 YGRRKRQRR 11

RESULT, 12
 AAY93542
 ID AAY93542 standard; peptide; 11 AA.
 XX
 AC AAY93542;
 XX
 XX 25-SEP-2000 (first entry)
 DT
 DT
 XX
 XX Amino acid sequence of a synthetic protein transduction domain.
 DE
 XX Protein transduction system; protein transduction domain;
 KM cytotoxic domain; pathogen infection; retroviral infection;
 KM plasmidial infection; cancer; prostate cancer.
 KM

PT diagnosis, prevention and treatment of diseases, disorders or
 PT conditions involving the central nervous system, teeth, heart, liver or
 PT adipose tissue -
 XX
 PS Disclosure: Page 62; 116pp; English.
 CC The present invention relates to new isolated fibroblast growth
 CC factor-like (FGF-L) nucleic acid molecules and polypeptides. The FGF-L
 CC polypeptide is useful for determining whether a compound inhibits FGF-L
 CC polypeptide, and also for identifying a compound that binds to the
 CC polypeptide. The FGF-L polypeptides of the invention are useful for
 CC treating, preventing or ameliorating a medical condition or an FGF-L
 CC polypeptide-related disease, condition or disorder such as wound healing
 CC disorders, ulcers, gut disorders, lung disorders, liver disorders such as
 CC hepatitis and diabetes. The invention is also useful for diagnosing a
 CC pathological condition or susceptibility to a pathological condition in
 CC a subject and is useful for modulating levels of FGF-L in an animal.
 CC Other uses are detecting or quantifying the amount of FGF-L polypeptide
 CC and for identifying or developing novel agonists and antagonists of the
 CC FGF-L polypeptide signalling pathway which are useful for treating one
 CC or more diseases or disorders, and also as an immunogen for producing
 CC antibodies for in vivo imaging. The present sequence represents an 11
 CC amino acid sequence from the human immunodeficiency virus (HIV) tat
 CC protein that is termed the protein transduction domain or TAT PPT.
 CC
 XX
 SQ Sequence 11 AA:
 Query Match 84.5%; Score 49; DB 22; Length 11;
 Best Local Similarity 72.7%; Pred. No. 0.12;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 YGRKKRRQKK 11
 Db 1 ygrkkrrqrrr 11
 RESULT 15
 AAU09812
 ID AAU09812 standard; Protein; 11 AA.
 XX
 AC AAU09812;
 XX
 DT 27-FEB-2002 (first entry)
 DE
 XX
 DE HIV-1 tat protein transduction domain (TAT PPT).
 XX
 KW fibroblast growth factor receptor-like protein; FGF-R; anorectic;
 KW haemostatic; osteopathic; cytostatic; nephrotoxic; antidiabetic;
 KW immunomodulator; antiinflammatory; haematopoietic disorder; osteoporosis;
 KW osteogenesis imperfecta; Paget's disease; periodontal disease; cancer;
 KW hypercalcaemia; acute glomerulonephritis; chronic glomerulonephritis;
 KW diabetes; obesity; cachexia; transgenic animal; gene therapy;
 KW human immunodeficiency virus; HIV-1; tat protein.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WC200170977-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 22-MAR-2001; 2001MO-US09073.
 XX
 PR 22-MAR-2000; 2000US-191379P.
 XX
 PA (AMGE-) AMGEN INC.
 PA (SARI/) SARIS C M.
 PA (MUSX/) MU S X.
 PA (XTAK/) XIA M.
 PA (FNON/) BOONE T C.
 PA (COVE/) COVEY T.
 XX
 PI Saris CM, Mu SX, Xia M, Boone TC, Covey T;

XX
 DR WPI: 2001-626128/72.
 XX
 PT Novel nucleic acid encoding fibroblast growth factor receptor-like
 PT polypeptides, useful for treating hematopoietic disorder, osteoporosis,
 PT Paget's disease, glomerulonephritis, cancer, diabetes, obesity and
 PT cachexia -
 XX
 PS Disclosure: Page 59; 163pp; English.
 CC
 XX The invention relates to a novel isolated fibroblast growth factor
 CC receptor-like (FGF-R) polypeptide (I). (I) and the nucleic acid (II)
 CC encoding (I) are useful for treating, preventing or ameliorating
 CC a medical condition including hematopoietic disorder, osteoporosis,
 CC osteogenesis imperfecta, Paget's disease, periodontal disease,
 CC hypercalcaemia, acute glomerulonephritis, chronic glomerulonephritis,
 CC cancer, diabetes, obesity and cachexia. (I) is also useful for
 CC identifying a compound which binds to FGF-R polypeptide, by contacting
 CC (I) with a compound, determining the extent of binding of the FGF-R
 CC polypeptide to the compound, and determining the activity of the
 CC polypeptide when bound to the compound. (II) is useful for modulating
 CC levels of a polypeptide in an animal. A transgenic animal comprising (I)
 CC is useful for determining whether a compound inhibits FGF-R polypeptide
 CC activity or FGF-R polypeptide production, by exposing the transgenic
 CC animal to the compound and measuring FGF-R polypeptide or production in
 CC the animal. (II) is useful for mapping the locations of FGF-R gene and
 CC related genes on chromosomes, as hybridisation probes in diagnostic
 CC assays to test for the presence of an FGF-R nucleic acid molecule in
 CC mammalian tissue or bodily fluid samples, in gene therapy, and as tools
 CC for isolating corresponding FGF-R polypeptide genes. (I) is useful as
 CC immunogen, and for cloning FGF-R polypeptide ligands using an
 CC expression cloning strategy. The present sequence represents the
 CC amino acid sequence of human immunodeficiency virus (HIV-1) tat protein
 CC transduction domain (TAT PPT) as described in the invention.
 CC
 XX
 SQ Sequence 11 AA:
 Query Match 84.5%; Score 49; DB 22; Length 11;
 Best Local Similarity 72.7%; Pred. No. 0.12;
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 YGRKKRRQKK 11
 Db 1 ygrkkrrqrrr 11
 Search completed: July 15, 2002, 12:57:59
 Job time: 415 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 12:59:19 ; Search time 75.67 seconds
(without alignments)
3.551 Million cell updates/sec

Title: US-09-712-819A-8

Perfect score: 58

Sequence: 1 YGRRKRROKK 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

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- 2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
- 3: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*
- 4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
- 5: /cgn2_6/prodata/2/1aa/PCITUS.COMB.pep:*
- 6: /cgn2_6/prodata/2/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	84.5	11	2	US-08-706-741B-54
2	49	84.5	11	2	US-08-924-695A-54
3	49	84.5	11	4	US-09-208-966-2
4	49	84.5	11	4	US-09-296-089-37
5	49	84.5	12	1	US-08-450-257-47
6	49	84.5	12	1	US-08-450-246-47
7	49	84.5	12	1	US-08-451-233-47
8	49	84.5	12	1	US-08-450-098-47
9	49	84.5	12	1	US-08-450-236-47
10	49	84.5	12	2	US-08-733-505A-50
11	49	84.5	12	4	US-08-235-403-47
12	49	84.5	14	5	PCT-US95-06077-4
13	49	84.5	14	5	PCT-US95-06077-10
14	49	84.5	14	5	PCT-US95-06077-11
15	49	84.5	15	5	PCT-US95-06077-12
16	49	84.5	15	1	US-08-450-257-5
17	49	84.5	15	1	US-08-450-257-5
18	49	84.5	15	1	US-08-450-246-5
19	49	84.5	15	1	US-08-450-246-6
20	49	84.5	15	1	US-08-450-098-6
21	49	84.5	15	1	US-08-451-233-5
22	49	84.5	15	1	US-08-451-233-6
23	49	84.5	15	1	US-08-450-236-5
24	49	84.5	15	1	US-08-450-236-6
25	49	84.5	15	4	US-08-235-403-5
26	49	84.5	15	4	US-08-235-403-5
27	49	84.5	15	4	US-08-235-403-6

28	49	84.5	17	2	US-08-902-623-7	Sequence 7, Appl
29	49	84.5	18	5	PCT-US95-06077-3	Sequence 3, Appl
30	49	84.5	21	1	US-08-450-257-50	Sequence 50, Appl
31	49	84.5	21	1	US-08-450-246-50	Sequence 50, Appl
32	49	84.5	21	1	US-08-450-098-50	Sequence 50, Appl
33	49	84.5	21	1	US-08-451-233-50	Sequence 50, Appl
34	49	84.5	21	1	US-08-450-236-50	Sequence 50, Appl
35	49	84.5	21	4	US-08-235-403-50	Sequence 50, Appl
36	49	84.5	22	1	US-08-450-257-3	Sequence 3, Appl
37	49	84.5	22	1	US-08-450-246-3	Sequence 3, Appl
38	49	84.5	22	1	US-08-450-098-3	Sequence 3, Appl
39	49	84.5	22	1	US-08-451-233-3	Sequence 3, Appl
40	49	84.5	22	1	US-08-450-236-3	Sequence 3, Appl
41	49	84.5	22	4	US-08-235-403-3	Sequence 3, Appl
42	49	84.5	24	1	US-08-450-257-4	Sequence 4, Appl
43	49	84.5	24	1	US-08-450-246-4	Sequence 4, Appl
44	49	84.5	24	1	US-08-450-098-4	Sequence 4, Appl
45	49	84.5	24	1	US-08-451-233-4	Sequence 4, Appl

ALIGNMENTS

```
RESULT 1
US-08-706-741B-54
; Sequence 54, Application US/08706741B
; Patent No. 5955593
;
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL, S. HAFERKAMP, L.C.
; STREET: 7733 FORKSTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63146
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,741B
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 965017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-706-741B-54

Query Match 84.5%; Score 49; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.067;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 YGRRKRROKK 11
Db 1 YGRRKRROKK 11
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RESULT 2
US-08-924-695A-54
; Sequence 54, Application US/08924695A
; Patent No. 5998583
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,695A
; FILING DATE: 09-SEP-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 971798
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-924-695A-54

Query Match      84.5%; Score 49; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.067;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRRKRROKKK 11
Db 1 YGRRKRROKKK 11

RESULT 3
US-09-208-966-2
; Sequence 2, Application US/09208966
; Patent No. 6221355
; GENERAL INFORMATION:
; APPLICANT: Dowdy, Steven F.
; TITLE OF INVENTION: ANTI-PATHOGEN SYSTEM AND METHODS OF USE THEREOF
; FILE REFERENCE: 48881/1742
; CURRENT APPLICATION NUMBER: US/09/208,966
; EARLIER FILING DATE: 1998-12-10
; EARLIER APPLICATION NUMBER: 60/082,402
; EARLIER FILING DATE: 1998-04-20
; EARLIER APPLICATION NUMBER: 60/069,012
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: human
US-09-208-966-2
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Query Match      84.5%; Score 49; DB 4; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.067;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRRKRROKKK 11
Db 1 YGRRKRROKKK 11

RESULT 4
US-09-296-089-37
; Sequence 37, Application US/09296089
; Patent No. 6303576
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Byers, Stephen
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: BETA-CATENIN MEDIATED GENE EXPRESSION
; FILE REFERENCE: 100086.411
; CURRENT APPLICATION NUMBER: US/09/296,089
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-296-089-37

Query Match      84.5%; Score 49; DB 4; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.067;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRRKRROKKK 11
Db 1 YGRRKRROKKK 11

RESULT 5
US-08-450-257-47
; Sequence 47, Application US/08450257
; Patent No. 5652122
; GENERAL INFORMATION:
; APPLICANT: FRANKEL, Alan
; APPLICANT: PABO, Carl
; APPLICANT: BARSDOM, James G.
; APPLICANT: FAMELL, Stephen E.
; APPLICANT: PERINSKY, R. B.
; TITLE OF INVENTION: TAY-DERIVED TRANSPORT POLYPEPTIDES
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,257
; FILING DATE: 25-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,403
; FILING DATE: 28-APR-1994
; APPLICATION NUMBER: US 07/934,375
; FILING DATE: 21-AUG-1992
```

APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-450-257-47

Query Match 84.5%; Score 49; DB 1; Length 12;
Best Local Similarity 72.7%; Pred. No. 0.072;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGKRRRQKK 11
|||||
DB 1 YGKRRRQRR 11

RESULT 6
US-08-450-246-47
Sequence 47, Application US/08450246
Patent No. 5670617
GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSON, James G.
APPLICANT: FAMEL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,246
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833

FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-450-246-47

Query Match 84.5%; Score 49; DB 1; Length 12;
Best Local Similarity 72.7%; Pred. No. 0.072;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGKRRRQKK 11
|||||
DB 1 YGKRRRQRR 11

RESULT 7
US-08-450-098-47
Sequence 47, Application US/08450098
Patent No. 5674980
GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSON, James G.
APPLICANT: FAMEL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,098
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989

APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8967
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-450-098-47

Query Match 84.5%; Score 49; DB 1; Length 12;
Best Local Similarity 72.7%; Pred. No. 0.072;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRRKKRRQKK 11
|||||
Db 1 YGRRKKRRQRR 11

RESULT 8
US-08-451-233-47
Sequence 47, Application US/08451233
Patent No. 5747641

GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOOM, James G.
APPLICANT: FAMELL, Stephen E.
APPLICANT: PEPIINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,233
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015

FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8967
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-451-233-47

Query Match 84.5%; Score 49; DB 1; Length 12;
Best Local Similarity 72.7%; Pred. No. 0.072;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGRRKKRRQKK 11
|||||
Db 1 YGRRKKRRQRR 11

RESULT 9
US-08-450-236-47
Sequence 47, Application US/08450236
Patent No. 5804604

GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOOM, James G.
APPLICANT: FAMELL, Stephen E.
APPLICANT: PEPIINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,236
FILING DATE: 25-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,403
FILING DATE: 28-APR-1994
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.

REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-450-236-47

Query Match 84.5%; Score 49; DB 1; Length 12;
Best Local Similarity 72.7%; Pred. No. 0.072;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGKRRRQKK 11
|||||:::
Db 1 YGKRRRQRR 11

RESULT 10
US-08-733-505A-50
Sequence 50, Application US/08733505A
Patent No. 3636445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-50

Query Match 84.5%; Score 49; DB 2; Length 12;
Best Local Similarity 72.7%; Pred. No. 0.072;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGKRRRQKK 11
|||||:::

Db 1 YGKRRRQRR 11

RESULT 11
US-08-235-403-47
Sequence 47, Application US/08235403
Patent No. 6316003
GENERAL INFORMATION:
APPLICANT: FRANKEL, Alan
APPLICANT: PABO, Carl
APPLICANT: BARSOUM, James G.
APPLICANT: FAWELL, Stephen E.
APPLICANT: PEPINSKY, R. B.
TITLE OF INVENTION: TAT-DERIVED TRANSPORT POLYPEPTIDES
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235,403
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,375
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/098,766
FILING DATE: 28-JUL-1993
APPLICATION NUMBER: PCT/US93/07833
FILING DATE: 19-AUG-1993
APPLICATION NUMBER: US 07/454,450
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: US 07/636,662
FILING DATE: 02-JAN-1991
APPLICATION NUMBER: US 08/158,015
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B170 CIP 2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-235-403-47

Query Match 84.5%; Score 49; DB 4; Length 12;
Best Local Similarity 72.7%; Pred. No. 0.072;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGKRRRQKK 11
|||||:::
Db 1 YGKRRRQRR 11

RESULT 12
PCT-US95-06077-4

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Sequence 4, Application PC/TUS9506077
GENERAL INFORMATION:
APPLICANT: Immunobiology Research, Institute Inc.
TITLE OF INVENTION: Vaccine Interdiction of Extracellular
TITLE OF INVENTION: Transactivating Proteins of Human Immunodeficiency Virus
TITLE OF INVENTION: and Other Chronically Infecting Viruses Employing Similar
TITLE OF INVENTION: Intercellular Transactivating Strategies
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06077
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/247,991
FILING DATE: 23-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: IR144PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US95-06077-4

Query Match      84.5%; Score 49; DB 5; Length 14;
Best Local Similarity 72.7%; Pred. No. 0.081;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy      1 YGRRKRROKK 11
Db      2 YGRRKRRORR 12

RESULT 13
PCT-US95-06077-10
Sequence 10, Application PC/TUS9506077
GENERAL INFORMATION:
APPLICANT: Immunobiology Research, Institute Inc.
TITLE OF INVENTION: Vaccine Interdiction of Extracellular
TITLE OF INVENTION: Transactivating Proteins of Human Immunodeficiency Virus
TITLE OF INVENTION: and Other Chronically Infecting Viruses Employing Similar
TITLE OF INVENTION: Intercellular Transactivating Strategies
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06077
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/247,991
FILING DATE: 23-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: IR144PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US95-06077-10

Query Match      84.5%; Score 49; DB 5; Length 14;
Best Local Similarity 72.7%; Pred. No. 0.081;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy      1 YGRRKRROKK 11
Db      2 YGRRKRRORR 12

RESULT 14
PCT-US95-06077-11
Sequence 11, Application PC/TUS9506077
GENERAL INFORMATION:
APPLICANT: Immunobiology Research, Institute Inc.
TITLE OF INVENTION: Vaccine Interdiction of Extracellular
TITLE OF INVENTION: Transactivating Proteins of Human Immunodeficiency Virus
TITLE OF INVENTION: and Other Chronically Infecting Viruses Employing Similar
TITLE OF INVENTION: Intercellular Transactivating Strategies
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06077
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/247,991
FILING DATE: 23-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: IR144PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
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MOLECULE TYPE: unknown
MOLECULE TYPE: peptide
PCT-US95-06077-11

Query Match 84.5%; Score 49; DB 5; Length 14;
Best Local Similarity 72.7%; Pred. No. 0.081;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRRRRQKK 11
Db 2 YGRRRRRQRR 12

RESULT 15
PCT-US95-06077-12
Sequence 12, Application PC/TUS9506077
GENERAL INFORMATION:
APPLICANT: Immunobiology Research, Institute Inc.
TITLE OF INVENTION: Vaccine Interdiction of Extracellular
TITLE OF INVENTION: Transactivating Proteins of Human Immunodeficiency Virus
TITLE OF INVENTION: and Other Chronically Infecting Viruses Employing Similar
TITLE OF INVENTION: Interleukin Transactivating Strategies
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06077
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/247,991
FILING DATE: 23-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: IR144PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
PCT-US95-06077-12

Query Match 84.5%; Score 49; DB 5; Length 14;
Best Local Similarity 72.7%; Pred. No. 0.081;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 YGRRRRRQKK 11
Db 2 YGRRRRRQRR 12

Search Completed: July 15, 2002, 12:59:20
Job time: 391 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 13:01:03 ; Search time 95.45 Seconds
(without alignments)
29.194 Million cell updates/sec

Title: US-09-712-819a-9

Perfect score: 144

Sequence: 1 YERRKRRQRRRSGGDTFTLTISLQAE D 29

Scoring table:

BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pirl:.*
2: pirl:.*
3: pirl:.*
4: pirl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	87	60.4	2 S37533	Ig kappa chain V r
2	87	60.4	2 S37530	Ig kappa chain V r
3	87	60.4	2 S37529	Ig kappa chain V r
4	87	60.4	2 S37535	Ig kappa chain V r
5	87	60.4	2 S37531	Ig kappa chain V r
6	87	60.4	2 S37534	Ig kappa chain V r
7	87	60.4	2 S37532	Ig kappa chain V r
8	87	60.4	2 PH0869	Ig kappa chain V r
9	87	60.4	2 B34133	Ig kappa chain V r
10	87	60.4	2 A4138	Ig kappa chain V r
11	87	60.4	2 S30523	Ig kappa chain V r
12	87	60.4	2 S30520	Ig kappa chain V r
13	87	60.4	2 S34003	Ig kappa chain V r
14	87	60.4	2 S34002	Ig kappa chain V r
15	87	60.4	1 K4HULN	Ig kappa chain V r
16	87	60.4	1 S44116	Ig kappa chain V r
17	87	60.4	2 S51147	Ig kappa chain V r
18	87	60.4	1 K4HU	Ig kappa chain V r
19	87	60.4	2 S40364	Ig kappa chain V r
20	87	60.4	1 K4HUI	Ig kappa chain V r
21	87	60.4	1 K4HUI7	Ig kappa chain V r
22	87	60.4	2 S49531	Ig kappa chain V r
23	84	58.3	2 S24215	Ig kappa chain V r
24	84	58.3	81 PH1048	Ig kappa chain V r
25	84	58.3	97 A42575	Ig kappa chain V r
26	84	58.3	101 S25337	Ig kappa chain V r
27	84	58.3	101 PH1046	Ig kappa chain V r
28	84	58.3	102 A34153	Ig kappa chain V r
29	84	58.3	103 PH1050	Ig kappa chain V r

30	84	58.3	103 2 PH1051	Ig light chain V r
31	84	58.3	103 2 PH1052	Ig light chain V r
32	84	58.3	103 2 PH1054	Ig light chain V r
33	84	58.3	103 2 PH1047	Ig light chain V r
34	84	58.3	104 2 PH1053	Ig light chain V r
35	84	58.3	104 2 PH1101	Ig light chain V r
36	84	58.3	104 2 PH1102	Ig light chain V r
37	84	58.3	104 2 PH1103	Ig light chain V r
38	84	58.3	104 2 PH1104	Ig light chain V r
39	84	58.3	104 2 C30534	Ig kappa chain V r
40	84	58.3	105 2 A30534	Ig kappa chain V r
41	84	58.3	107 2 B30535	Ig kappa chain V r
42	84	58.3	107 2 G30535	Ig kappa chain V r
43	84	58.3	107 2 D30535	Ig kappa chain V r
44	84	58.3	107 2 F30535	Ig kappa chain V r
45	84	58.3	107 2 S36268	Ig lambda chain V

ALIGNMENTS

RESULT 1
S37533
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37533
R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)-ID(+) cells, the major B cell subset in the peripheral bl
A:Reference number: S37501
A:Accession: S37533
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:226627; NID:9405708; PTDN:CAA81380.1; PID:9405709
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 60.4%; Score 87; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 SGGCTDFTLTISLQAE D 29
Db 49 SGGCTDFTLTISLQAE D 66
RESULT 2
S37530
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37530
R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)-ID(+) cells, the major B cell subset in the peripheral bl
A:Reference number: S37501
A:Accession: S37530
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:226630; NID:9405702; PTDN:CAA81383.1; PID:9405703
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 60.4%; Score 87; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 SGGCTDFTLTISLQAE D 29

Db 49 SGSGTDFTLTSSLSQAED 66

RESULT 3

Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37529
R:Klein, U.; Kuipers, R.; Rajewsky, K.
Submitted to the EMBL Data Library, September 1993
A:Description: Human IgM(+)19D(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37529
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:226631; NID:g405700; PIDN:CAA81384.1; PID:g405701
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match 60.4%; Score 87; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SGSGTDFTLTSSLSQAED 29
Db 49 SGSGTDFTLTSSLSQAED 66

RESULT 4

Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37535
R:Klein, U.; Kuipers, R.; Rajewsky, K.
Submitted to the EMBL Data Library, September 1993
A:Description: Human IgM(+)19D(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37535
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:226625; NID:g405712; PIDN:CAA81378.1; PID:g405713
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match 60.4%; Score 87; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SGSGTDFTLTSSLSQAED 29
Db 49 SGSGTDFTLTSSLSQAED 66

RESULT 5

Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37531
R:Klein, U.; Kuipers, R.; Rajewsky, K.
Submitted to the EMBL Data Library, September 1993
A:Description: Human IgM(+)19D(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37531
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:226629; NID:g405704; PIDN:CAA81382.1; PID:g405705
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match 60.4%; Score 87; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SGSGTDFTLTSSLSQAED 29
Db 49 SGSGTDFTLTSSLSQAED 66

RESULT 6

Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37534
R:Klein, U.; Kuipers, R.; Rajewsky, K.
Submitted to the EMBL Data Library, September 1993
A:Description: Human IgM(+)19D(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37534
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:226626; NID:g405710; PIDN:CAA81379.1; PID:g405711
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match 60.4%; Score 87; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SGSGTDFTLTSSLSQAED 29
Db 49 SGSGTDFTLTSSLSQAED 66

RESULT 7

Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37532
R:Klein, U.; Kuipers, R.; Rajewsky, K.
Submitted to the EMBL Data Library, September 1993
A:Description: Human IgM(+)19D(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37532
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:226628; NID:g405706; PIDN:CAA81381.1; PID:g405707
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

Query Match 60.4%; Score 87; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SGSGTDFTLTSSLSQAED 29
Db 49 SGSGTDFTLTSSLSQAED 66

RESULT 8

PH0869

Ig kappa chain V region (anti-DNA, HZF) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C:Accession: PH0869
R:Manheimer-Loty, A.; Katz, J.B.; Pillingner, M.; Ghosssein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiootype
A:Reference number: PH0862; MUID:92078875
A:Accession: PH0869
A:Molecule type: DNA
A:Residues: 1-101 <MAN>
A>Note: residues 28-33 were obtained from Figure 4
C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-96/Domain: immunoglobulin homology <IMM>
F:24-40/Region: complementarity-determining 1
F:41-55/Region: complementarity-determining 2
F:56-62/Region: complementarity-determining 2
F:63-94/Region: framework 3
F:95-101/Region: complementarity-determining 3

Query Match 60.4%; Score 87; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGCTDFTLTITSSLOAED 29
DB 71 SSGCTDFTLTITSSLOAED 88

RESULT 9
B34153
Ig kappa chain V-IV region (Fue) - human
C:Species: Homo sapiens (man)
C>Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jan-2000
C:Accession: B34153
R:Maniaco, E.; Ayadi, H.; Conroy, N.; Gendron, M.C.; Roy, J.P.; Heyermann, H.; Frangione
J. Biol. Chem. 264, 21481-21485, 1989
A:Title: Multiple mutations in the variable region of the kappa light chains of three mc
A:Reference number: A34153; MUID:90094913
A:Accession: B34153
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-102 <MTH>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 60.4%; Score 87; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGCTDFTLTITSSLOAED 29
DB 71 SSGCTDFTLTITSSLOAED 88

RESULT 10
A49138
IgA kappa rheumatoid factor variable - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A49138
R:Gause, A.; Kupperts, R.; Mierau, R.
Clin. Exp. Immunol. 88, 430-434, 1992
A:Title: A somatically mutated V kappa IV gene encoding a human rheumatoid factor light
A:Reference number: A49138; MUID:92298590
A:Accession: A49138
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-106 <GAD>
A:Cross-references: GB:S37926; NID:9298207; PIDN:AA822366.1; PID:9298208
A>Note: sequence inconsistent with the nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIN:106633, NCBIIP:106637)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:20-99/Domain: immunoglobulin homology <IMM>

Query Match 60.4%; Score 87; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGCTDFTLTITSSLOAED 29
DB 74 SSGCTDFTLTITSSLOAED 91

RESULT 11
S30523
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S30523
R:Marlette, X.
Submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30523
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAR>
A:Cross-references: EMBL:Z18329
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 60.4%; Score 87; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGCTDFTLTITSSLOAED 29
DB 71 SSGCTDFTLTITSSLOAED 88

RESULT 12
S30520
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S30520
R:Marlette, X.
Submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30520
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAR>
A:Cross-references: EMBL:Z18325
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 60.4%; Score 87; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGCTDFTLTITSSLOAED 29
DB 71 SSGCTDFTLTITSSLOAED 88

RESULT 13

S34003
 Ig kappa chain V region - human
 C:Species: Homo sapiens (man)
 C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S34003
 R:Marlette, X.; Tsapis, A.; Brouet, J.C.
 Eur. J. Immunol. 23, 846-851, 1993
 A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
 A:Keywords: heterotrimer; immunoglobulin
 A:Accession: S34001; MUID:93209281
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-113 <MAR>
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:16-96/Domain: immunoglobulin homology <IMM>

Query Match

60.4%; Score 87; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 0.00013;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SGSGTDFTLTISLQAE 29

|||||

Db 71 SGSGTDFTLTISLQAE 88

RESULT 14

S34002

Ig kappa chain V region - human
 C:Species: Homo sapiens (man)
 C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
 C:Accession: S34002; S30522
 R:Marlette, X.; Tsapis, A.; Brouet, J.C.
 Eur. J. Immunol. 23, 846-851, 1993
 A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
 A:Reference number: S34001; MUID:93209281
 A:Accession: S34002
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-113 <MAR>
 A:Cross-references: EMBL:218328
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:16-96/Domain: immunoglobulin homology <IMM>

Query Match

60.4%; Score 87; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 0.00013;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SGSGTDFTLTISLQAE 29

|||||

Db 71 SGSGTDFTLTISLQAE 88

RESULT 15

KAHULN

Ig kappa chain V-IV region (Len) - human
 C:Species: Homo sapiens (man)
 C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 01-Dec-2000
 C:Accession: A01903; F61458
 R:Schneider, M.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 356, 507-557, 1975
 A:Title: Die Primärstruktur einer monoklonalen Immunoglobulin-L-Kette der Subgruppe IV
 A:Reference number: A01903; MUID:76004342
 A:Accession: A01903
 A:Molecule type: protein
 A:Residues: 1-114 <SCH>
 A:Note: this is the first completely sequenced V region of a new kappa chain subgroup.
 A:Note: the C-region of this chain has the Inv (3) marker

R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Minaresco, E.
 J. Exp. Med. 170, 1551-1558, 1989

A:Title: Expression of a public idotype by human monoclonal IGM directed to myelin-a
 A:Reference number: A61458; MUID:90039128

A:Accession: F61458

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <ARO>

C:Comment: This is a Bence Jones protein.

C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

F:23-94/Disulfide bonds: #status predicted

Query Match

60.4%; Score 87; DB 1; Length 114;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SGSGTDFTLTISLQAE 29

|||||

Db 71 SGSGTDFTLTISLQAE 88

Search completed: July 15, 2002, 13:01:03
 Job time: 469 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 13:23:34 : Search time 44.9 Seconds

(without alignments)
25,008 Million cell updates/sec

Title: US-09-712-819A-9

Sequence: 1 YERKKRRQRRSGTGDTFTLTSSLOAED 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt-40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	87	60.4	114	KV4A_HUMAN	P01625 homo sapien
2	87	60.4	121	KV4B_HUMAN	P06312 homo sapien
3	87	60.4	133	KV4B_HUMAN	P06313 homo sapien
4	87	60.4	134	KV4C_HUMAN	P06314 homo sapien
5	82	56.9	108	KV4H_HUMAN	P01600 homo sapien
6	82	56.9	116	KV3J_HUMAN	P04434 homo sapien
7	82	56.9	117	KV3I_HUMAN	P01601 homo sapien
8	82	56.9	129	KV1W_HUMAN	P04431 homo sapien
9	80	55.6	109	KV3F_HUMAN	P01624 homo sapien
10	80	55.6	114	KV3A_MOUSE	P01632 mus musculu
11	80	55.6	149	KV5A_MOUSE	P01633 mus musculu
12	79	54.9	108	KV1O_HUMAN	P01609 homo sapien
13	79	54.9	115	KV3I_HUMAN	P04433 homo sapien
14	78	54.2	108	KV1M_HUMAN	P01611 homo sapien
15	78	54.2	108	KV1S_HUMAN	P01611 homo sapien
16	78	54.2	108	KV1V_HUMAN	P01611 homo sapien
17	78	54.2	108	KV1V_HUMAN	P01611 homo sapien
18	76	52.8	108	KV5B_MOUSE	P01634 mus musculu
19	76	52.8	108	KV1V_HUMAN	P01595 homo sapien
20	75	52.1	108	KV1F_HUMAN	P01598 homo sapien
21	75	52.1	108	KV1G_HUMAN	P01598 homo sapien
22	75	52.1	108	KV1O_HUMAN	P01607 homo sapien
23	75	52.1	108	KV1P_HUMAN	P01608 homo sapien
24	75	52.1	108	KV1R_HUMAN	P01610 homo sapien
25	75	52.1	117	KV1J_HUMAN	P01610 homo sapien
26	75	52.1	129	KV3H_HUMAN	P04207 homo sapien
27	74	51.4	107	KV1D_HUMAN	P01596 homo sapien
28	74	51.4	109	KV3D_HUMAN	P01622 homo sapien
29	74	51.4	109	KV3E_HUMAN	P01623 homo sapien
30	74	51.4	109	KV3G_HUMAN	P04206 homo sapien
31	74	51.4	129	KV3L_HUMAN	P18135 homo sapien
32	73	50.7	107	KV04_RAB1T	P01685 oryctolagus
33	73	50.7	115	KV2A_HUMAN	P01614 homo sapien

34	73	50.7	129	1	KV1X_HUMAN	P04432 homo sapien
35	72	50.0	108	1	KV1L_HUMAN	P01604 homo sapien
36	71	49.3	108	1	KV1E_HUMAN	P01597 homo sapien
37	71	49.3	108	1	KV1N_HUMAN	P01620 homo sapien
38	71	49.3	109	1	KV3B_HUMAN	P01620 homo sapien
39	71	49.3	109	1	KV5I_MOUSE	P01642 mus musculu
40	70	48.6	108	1	KV06_RAB1T	P01687 oryctolagus
41	70	48.6	108	1	KV3A_HUMAN	P01619 homo sapien
42	70	48.6	109	1	KV1T_HUMAN	P01612 homo sapien
43	70	48.6	112	1	KV2D_MOUSE	P01629 mus musculu
44	70	48.6	113	1	KV2B_HUMAN	P01615 homo sapien
45	70	48.6	113	1	KV2D_HUMAN	P01617 homo sapien

ALIGNMENTS

```
RESULT 1
ID      KV4A_HUMAN      STANDARD;      PRT;      114 AA.
AC      P01625;
DT      21-JUL-1986 (Rel. 01, Created)
DR      01-OCT-1996 (Rel. 34, Last sequence update)
DE      15-JUN-1999 (Rel. 38, Last annotation update)
DE      Ig kappa chain V-IV region Len.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      MEDLINE=76004342; PubMed=50995;
RX      Schneider M., Hilschmann N.;
RT      "The primary structure of a monoclonic immunoglobulin-L-chain of
RT      subgroup IV of the kappa type (Bence-Jones protein Len).";
RL      Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
RN      [2]
RP      Revision TO 9.
RA      Salomon A.;
RL      Submitted (AUG-1996) to the SWISS-PROT data bank.
CC      -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR      PIR; A01903; K4HJLN.
DR      HSSP; P01789; IMCP.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003596; Ig_V.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
KW      Immunoglobulin V region; Bence-Jones protein.
FT      DOMAIN 1 23
FT      DOMAIN 2 40
FT      DOMAIN 3 55
FT      DOMAIN 4 62
FT      DOMAIN 5 94
FT      DOMAIN 6 101
FT      DOMAIN 7 102
FT      DISULFID 23 94
FT      NON_TER 114
SQ      SEQUENCE 114 AA; 12640 MW; 06471D17F736485 CRC64;
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Query Match 60.4%; Score 87; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 4,9e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SGGSGTPTFTLTSSLOAED 29
DB 71 SGGSGTPTFTLTSSLOAED 88

RESULT 2
KV4O_HUMAN STANDARD; PRT; 121 AA.
ID KV4O_HUMAN

```

AC P06312;
DT 01-JAN-1988 (Rel. 06, Created)
DE 15-JUL-1999 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Comblato G., Mocikat R., Pohlentz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene."
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -1- MISCELLANEOUS: THERE IS ONLY ONE IG KAPPA V-IV GENE.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: 200023; CAA77318.1; -.
CC PIR: A01902; K4HU.
CC HSSP: P01789; IMCP.
CC InterPro: IPR003006; IG_MHC.
CC InterPro: IPR003596; IG-V.
CC Pfam: PF00047; Ig_1.
CC SMART: SM00406; IGV_1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >121 IG KAPPA CHAIN V-IV REGION.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13380 MW; 9586AD4180D33974 CRC64;

Query Match 60.4%; Score 87; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SGGSTDFLTITISLQAE 29
DB 91 SGGSTDFLTITISLQAE 108

RESULT 3
KV4B_HUMAN STANDARD; PRT; 133 AA.
ID KV4B_HUMAN
AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Comblato G., Mocikat R., Pohlentz H.D.,

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RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene."
RL Nucleic Acids Res. 13:6515-6529(1985).
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CC -----
CC EMBL: 200022; CAA77317.1; -.
CC PIR: A01904; K4HUI.
CC HSSP: P01789; IMCP.
CC InterPro: IPR003006; IG_MHC.
CC InterPro: IPR003596; IG-V.
CC Pfam: PF00047; Ig_1.
CC SMART: SM00406; IGV_1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 IG KAPPA CHAIN V-IV REGION JI.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 122 FRAMEWORK-4.
FT DOMAIN 123 132 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match 60.4%; Score 87; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SGGSTDFLTITISLQAE 29
DB 91 SGGSTDFLTITISLQAE 108

RESULT 4
KV4C_HUMAN STANDARD; PRT; 134 AA.
ID KV4C_HUMAN
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned
RT cDNA probe."
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
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CC EMBL; X02990; CAA26733.1; -

CC PIR; A01905; K4H017.

DR HSSP; P01789; IMCP.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; Ig; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20

FT CHAIN 21 134

FT DOMAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.

FT DOMAIN 21 43 FRAMEWORK-1.

FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 61 75 FRAMEWORK-2.

FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 83 114 FRAMEWORK-3.

FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 122 133 FRAMEWORK-4.

FT DISULFID 43 114 BY SIMILARITY.

FT NON_TER 134 134

SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match Best Local Similarity 60.4%; Score 87; DB 1; Length 134; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSTDFLTITSSLOAED 29

DB 91 SSGSTDFLTITSSLOAED 108

|||||

RESULT 5

KVII_HUMAN STANDARD; PRT; 108 AA.

ID KVII_HUMAN

AC P01600;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-I region Hau.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCBI_TaxID=9606;

OX NCBI_TaxID=9606;

RM [1]

RP SEQUENCE.

RX MEDLINE-71032830; PubMed-4097974;

RA Matanabe S., Hilschmann N.;

RT "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): a subdivision within RT subgroups."

RT Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

DR PIR; A01868; KIHUHU.

DR HSSP; P80362; IMTL.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; Ig; 1.

KW Immunoglobulin V region; Bence-Jones protein.

FT DOMAIN 1 23 FRAMEWORK-1.

FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 35 49 FRAMEWORK-2.

FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 57 88 FRAMEWORK-3.

FT DOMAIN 89 97 FRAMEWORK-4.

FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.

FT DISULFID 23 88 BY SIMILARITY.

FT NON_TER 108 108

SQ SEQUENCE 108 AA; 11671 MW; 08D3A616D8D0618 CRC64;

Query Match Best Local Similarity 56.9%; Score 82; DB 1; Length 108; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 SSGSTDFLTITSSLOAED 29

DB 65 SSGSTDFLTITSSLOAED 82

|||||

RESULT 6

KV3J_HUMAN STANDARD; PRT; 116 AA.

ID KV3J_HUMAN

AC P04434;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-III region VH precursor (fragment).

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OC NCBI_TaxID=9606;

OX NCBI_TaxID=9606;

RM [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-85087932; PubMed-6440122;

RA Peck M., Zachau H.G.;

RT "Immunoglobulin genes of different subgroups are interdigitated within the VK locus."

RL Nucleic Acids Res. 12:9229-9236(1984).

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CC -----

DR EMBL; X02725; -; NOT_ANNOTATED_CDS.

DR PIR; A01901; K3H0VH.

DR HSSP; P01789; 2MCP.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; Ig; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20

FT CHAIN 21 >116

FT DOMAIN 21 43 FRAMEWORK-1.

FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 56 70 FRAMEWORK-2.

FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 78 109 FRAMEWORK-3.

FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING-3.

FT DISULFID 43 109 BY SIMILARITY.

FT NON_TER 116 116

SQ SEQUENCE 116 AA; 12757 MW; 51CD5BA53B21929 CRC64;

Query Match Best Local Similarity 56.9%; Score 82; DB 1; Length 116; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 12 SSGSTDFLTITSSLOAED 29

DB 86 SSGSTDFLTITSSLOAED 103

|||||

RESULT 7

KVII_HUMAN STANDARD; PRT; 117 AA.

ID KVII_HUMAN

AC P01601;

```
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region HK101 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81098966; PubMed=6779204;
RA Bentley D.L., Rabbitts T.H.;
RT "Human immunoglobulin variable region genes -- DNA sequences of two V
RL Nature 288:730-733(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83129397; PubMed=6402305;
RA Bentley D.L., Rabbitts T.H.;
RT "Evolution of immunoglobulin V genes: evidence indicating that
RT recently duplicated human V kappa sequences have diverged by gene
RT conversion."
RL Cell 32:181-189(1983).
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CC -----
DR EMBL; K01322; AAA58930.1; -
DR EMBL; K01324; AAA58932.1; -
DR EMBL; V00558; CAA23824.1; -
DR PIR; A01881; K1H011.
DR PIR; A21056; A21056.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 >117 IG KAPPA CHAIN V-I REGION HK101.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12799 MW; D7D0FF3718CEP587 CRC64;
```

```
Query Match 56.9%; Score 82; DB 1; Length 117;
Best Local Similarity 94.4%; Pred. No. 2.7e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 12 SGGSTDFLTITSSLOAED 29
DB 87 SGGSTDFLTITSSLOPED 104
```

```
RESULT 8
ID K1YM_HUMAN STANDARD; PRT; 129 AA.
AC P04431.
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
```

```
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8501418; PubMed=6091049;
RA Klobbeck H.G., Combiato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL lymphoid cell lines are closely related."
RL Nucleic Acids Res. 12:6995-7006(1984).
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CC -----
DR EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; K1H0WK.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AEC2P9 CRC64;
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```
Query Match 56.9%; Score 82; DB 1; Length 129;
Best Local Similarity 94.4%; Pred. No. 3.1e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
OY 12 SGGSTDFLTITSSLOAED 29
DB 87 SGGSTDFLTITSSLOPED 104
```

```
RESULT 9
ID K1YF_HUMAN STANDARD; PRT; 109 AA.
AC P01624.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig kappa chain V-II region POW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76276460; PubMed=60899;
RA Klapper D.G., Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains
RT from two idiotypically cross reactive IGM anti-gamma globulins."
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC -I- MYSCLELANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01897; K3H0PM.
```

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DR HSP: P01789; 2MCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
DISULFID 23 89
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;

Query Match 55.6%; Score 80; DB 1; Length 109;
Best Local Similarity 88.9%; Pred. No. 5e-05;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGCTDFLTITSSLOAED 29
DB 66 SSGCTDFLTITSSLOAED 83

RESULT 10
KVLA_MOUSE STANDARD; PRT; 114 AA.
ID P01632;
AC P01632;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region S107A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81241357; PubMed=6788890;
RA Kwan S.-P., Rudnikoff S., Seidman J.G., Leder P., Scharff M.D.;
RT "Nucleic acid and protein sequences of phosphocholine-binding light
RT chains."
RL J. Exp. Med. 153:1366-1370(1981).
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CC -----
DR EMBL: U29423; AAC00033.1; -.
DR PIR: A01915; KVM57A.
DR HSP: P01789; 1MCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
DISULFID 1 23
FT DOMAIN 24 40 FRAMEWORK-1.
FT DOMAIN 41 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 62 FRAMEWORK-2.
FT DOMAIN 63 94 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 95 103 FRAMEWORK-3.
FT DOMAIN 104 113 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 94 FRAMEWORK-4.
FT NON_TER 114 114 BY SIMILARITY.
SQ SEQUENCE 114 AA; 12717 MW; 32008EC8E9DE67B CRC64;

Query Match 55.6%; Score 80; DB 1; Length 114;
Best Local Similarity 88.9%; Pred. No. 5.2e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 SSGCTDFLTITSSLOAED 29

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DB 71 SSGCTDFLTITSSLOAED 88

RESULT 11
KVLA_MOUSE STANDARD; PRT; 149 AA.
ID KVLA_MOUSE
AC P01633;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region MPC11 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-71 FROM N.A.
RX MEDLINE=83001944; PubMed=6288267;
RA Kelley D.E., Coleclough C., Perry R.P.;
RT "Functional significance and evolutionary development of the
RT 5'-terminal regions of immunoglobulin variable-region genes."
RL Cell 29:681-689(1982).
RN [2]
RP SEQUENCE OF 41-149 FROM N.A.
RX MEDLINE=80176554; PubMed=6245773;
RA Rabbitts T.H., Hamlyn P.H., Mathysens G., Roe B.A.;
RT "The variability, arrangement, and rearrangement of immunoglobulin
RT genes."
RL Can. J. Biochem. 58:176-187(1980).
RN [3]
RP SEQUENCE OF 30-149.
RX MEDLINE=78186617; PubMed=418775;
RA Smith G.P.;
RT "Sequence of the full-length immunoglobulin kappa-chain of mouse
RT myeloma MPC 11."
RL Biochem. J. 171:337-347(1978).
CC -1- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS
CC AMINO END, DUE TO A TANDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE
CC CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL
CC RESIDUE OF TYPICAL KAPPA CHAINS.
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CC -----
DR EMBL: J00561; AAA38776.1; -.
DR PIR: A01916; KVM511.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal; Repeat.
DISULFID 1 29
FT CHAIN 30 149 IG KAPPA CHAIN V-V REGION MPC11.
FT DOMAIN 42 64 FRAMEWORK-1.
FT DOMAIN 65 75 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 76 90 FRAMEWORK-2.
FT DOMAIN 91 97 FRAMEWORK-3.
FT DOMAIN 98 129 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 130 138 FRAMEWORK-3.
FT DOMAIN 139 148 COMPLEMENTARITY-DETERMINING-3.
FT REPEAT 26 35 FRAMEWORK-4.
FT REPEAT 36 47
FT NON_TER 149 149
SQ SEQUENCE 149 AA; 16434 MW; B0480C87B682AC3E CRC64;

Query Match 55.6%; Score 80; DB 1; Length 149;

```


Search completed: July 15, 2002, 13:23:34
 Job time: 1450 sec

DR Pfam: PF00047; Ig: 1.
 DR SMART: SM00406; IGV: 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34 FRAMEWORK-1.
 FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 50 56 FRAMEWORK-2.
 FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 89 97 FRAMEWORK-3.
 FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 23 88 FRAMEWORK-4.
 FT NON_TER 108 88 BY SIMILARITY.
 SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 54.2%; Score 78; DB 1; Length 108;
 Best Local Similarity 88.9%; Pred. No. 9,7e-05;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 12 SGGSTDFTLTISSLAQAD 29
 ||||| ||||| ||
 DB 65 SGGSTDFTLTISSLAQPED 82

RESULT 15
 ID KY1S_HUMAN STANDARD; PRT: 108 AA.
 AC P01611;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Wes.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-81092279; PubMed-6778806;
 RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
 RT "Preparative separation of the tryptic hydrolysate of a protein by
 RT high-pressure liquid chromatography. The primary structure of a
 RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
 Wes).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1596(1980).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR: A01877; KIHUWS.
 DR HSSP: P80362; IWTL.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig: 1.
 DR SMART: SM00406; IGV: 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 88
 SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match 54.2%; Score 78; DB 1; Length 108;
 Best Local Similarity 88.9%; Pred. No. 9,7e-05;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 SGGSTDFTLTISSLAQAD 29
 ||||| ||||| ||
 DB 65 SGGSTDFTLTISSLAQPED 82

10

11

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OK protein - protein search, using sw model

Run on: July 15, 2002, 13:22:47 ; Search time 172.49 Seconds
(without alignments)
29.085 Million cell updates/sec

Title: US-09-712-819A-9

Sequence: 1 YEKRRRQRRRSGTDFLTITSLQAE 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	57.6	107	4 Q9UL81	Q9UL81 homo sapien
2	82	56.9	107	4 Q96SA9	Q96SA9 homo sapien
3	82	56.9	108	4 Q9UL77	Q9UL77 homo sapien
4	82	56.9	108	4 Q9UL70	Q9UL70 homo sapien
5	80	55.6	107	11 Q9ER29	Q9ER29 mus musculu
6	80	55.6	109	4 Q9UL85	Q9UL85 homo sapien
7	79	54.9	108	4 Q9UL79	Q9UL79 homo sapien
8	77	53.5	108	4 Q9UL83	Q9UL83 homo sapien
9	74	51.4	109	4 Q9UL78	Q9UL78 homo sapien
10	73	50.7	109	6 Q9N0W5	Q9N0W5 oryctolagus
11	71	49.3	99	11 Q9UL74	Q9UL74 mus musculu
12	70	48.6	104	11 Q9UL82	Q9UL82 mus musculu
13	70	48.6	114	4 Q9UL80	Q9UL80 homo sapien
14	70	48.6	238	11 Q9NM37	Q9NM37 mus musculu
15	69	47.9	233	11 Q9LWS9	Q9LWS9 mus musculu
16	69	47.9	234	11 Q9LWF8	Q9LWF8 mus musculu

17	66	45.8	109	4 Q9UL86	Q9UL86 homo sapien
18	66	45.8	235	11 Q9LW12	Q9LW12 mus musculu
19	65	45.1	214	11 Q9RIA5	Q9RIA5 mus musculu
20	64	44.4	106	5 Q9UL40	Q9UL40 schistosoma
21	64	44.4	107	11 Q9JL84	Q9JL84 mus musculu
22	64	44.4	116	4 Q96PF6	Q96PF6 homo sapien
23	63	43.8	97	11 Q9JL76	Q9JL76 mus musculu
24	63	43.8	127	11 Q9ZSS9	Q9ZSS9 mus musculu
25	62	43.1	71	15 Q40Z31	Q40Z31 human
26	62	43.1	101	11 Q9JL78	Q9JL78 mus musculu
27	62	43.1	211	11 Q9JLX0	Q9JLX0 mus musculu
28	61	42.4	111	11 Q9Z0E9	Q9Z0E9 mus musculu
29	60	41.7	72	15 P90117	P90117 human
30	60	41.7	109	11 Q9Z0E6	Q9Z0E6 mus musculu
31	60	41.7	298	11 Q90YF0	Q90YF0 mus musculu
32	59	41.0	72	15 P90128	P90128 human
33	59	41.0	101	15 Q90ZM7	Q90ZM7 human
34	59	41.0	101	15 Q90ZL7	Q90ZL7 human
35	58	40.3	72	15 P90118	P90118 human
36	58	40.3	101	15 Q90ZP1	Q90ZP1 human
37	58	40.3	399	10 Q9EY9	Q9EY9 oryza sativ
38	57.5	39.9	86	15 Q99BW1	Q99BW1 human
39	56	38.9	71	15 Q9JL04	Q9JL04 human
40	56	38.9	71	15 Q9JL03	Q9JL03 human
41	56	38.9	71	15 Q9JL07	Q9JL07 human
42	56	38.9	72	15 Q89T31	Q89T31 human
43	56	38.9	72	15 Q89T32	Q89T32 human
44	56	38.9	72	15 Q89T33	Q89T33 human
45	56	38.9	72	15 Q9WMS3	Q9WMS3 human

ALIGNMENTS

RESULT 1
ID Q9UL81 PRELIMINARY: PRT: 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035033; AAD56269.1; .
DR HSSP: P01607; IREI.
DR InterPro: IPR003066; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF00047; IG_1.
DR SMART: SM00406; IG_1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 57.6%; Score 83; DB 4; Length 107;

Best Local Similarity 94.4%; Pred. No. 3.2e-05;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 SSGSGTDFLTITSLQAE 29
DB 65 SSGSGTDFLTITSLQAE 82

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RESULT 2
ID Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL: U96396; AAB6785.1; -.
FT NON_TER 1 107
FT SEQUENCE 107 AA; 11520 MM; 4B43E9C5B577F16 CRC64;
SO

Query Match 56.9%; Score 82; DB 4; Length 107;
Best Local Similarity 94.4%; Pred. No. 4.5e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 SSGCTDFTLTSSLOAED 29
Db 65 SSGCTDFTLTSSLOPED 82

RESULT 3
ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035037; AAD56273.1; -.
FT NON_TER 1 108
FT SEQUENCE 108 AA; 11738 MM; C06681716C4D16F3 CRC64;
SO

Query Match 56.9%; Score 82; DB 4; Length 108;
Best Local Similarity 94.4%; Pred. No. 4.6e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 12 SSGCTDFTLTSSLOAED 29
Db 65 SSGCTDFTLTSSLOPED 82

RESULT 4
ID Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035044; AAD56280.1; -.
DR HSSP: P01607; IRET.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1 108
FT SEQUENCE 108 AA; 11633 MM; B7BEDC3E41FCCA37 CRC64;
SO

Query Match 56.9%; Score 82; DB 4; Length 108;
Best Local Similarity 94.4%; Pred. No. 4.6e-05;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 SSGCTDFTLTSSLOAED 29
Db 65 SSGCTDFTLTSSLOPED 82

RESULT 5
ID Q9ERZ9 PRELIMINARY; PRT; 107 AA.
AC Q9ERZ9;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
DE Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=70090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
RT "Cloning and sequencing of the light chain fragment of variable region
RT genes of an anti-TNF-a monoclonal antibody."
RL J. Cell. Mol. Immunol. 12:21-26(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Construction and sequencing of the single-chain antibody gene of a
RT human TNF-alpha specific monoclonal antibody."
RL T14 Chun I Ta Hsueh Hsueh Pao 19:373-376(1998).
RN [3]
RP SEQUENCE FROM N.A.
```

RA Cher P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
 RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF262753; AAG23804.1; -
 DR HSSP; P80362; IWT.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00409; Ig; 1.
 DR SMART: SM00406; Ig; 1.
 FT NON_TER 107 107
 SQ SEQUENCE 107 AA; 11784 MW; 2B15EBA604A26C3 CRC64;

Query Match 55.6%; Score 80; DB 11; Length 107;
 Best Local Similarity 88.9%; Pred. No. 9.2e-05;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 SSGSTDFLTITSSLOAED 29
 |||||
 DB 68 SSGSTDFLTITSSLOVED 85

RESULT 6
 OYUL85 PRELIMINARY; PRT: 109 AA.

AC OYUL85; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN KAPPA CHAIN VARIABLE REGION
 DE (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035029; AAD56265.1; -
 DR HSSP; P80362; IWT.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; Ig; 1.
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 55.6%; Score 80; DB 4; Length 109;
 Best Local Similarity 88.9%; Pred. No. 9.4e-05;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSTDFLTITSSLOAED 29
 |||||
 DB 65 SSGSTDFLTITSSLOSED 82

RESULT 7
 OYUL79 PRELIMINARY; PRT: 108 AA.

AC OYUL79; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
 DE (FRAGMENT).

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035035; AAD56271.1; -
 DR HSSP; P01607; IRET.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; Ig; 1.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 54.9%; Score 79; DB 4; Length 108;
 Best Local Similarity 88.9%; Pred. No. 0.00013;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 SSGSTDFLTITSSLOAED 29
 |||||
 DB 65 SSGSTDFLTITSSLOSED 82

RESULT 8
 OYUL83 PRELIMINARY; PRT: 108 AA.

AC OYUL83; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
 DE (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035031; AAD56267.1; -
 DR HSSP; P80362; IWT.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; Ig; 1.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EBA CRC64;

Query Match 53.5%; Score 77; DB 4; Length 108;
 Best Local Similarity 88.9%; Pred. No. 0.00027;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 SSGSTDFLTITSSLOAED 29
 |||||
 DB 65 SSGSTDFLTITSSLOFED 82

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RESULT 9
ID 09UL78 PRELIMINARY: PRT: 109 AA.
AC 09UL78;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
RL EMBL: AF035036; AAD56272.1; -.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA: 11646 MW: 5f675c52ec7e197 CRC64;

Query Match 51.4%; Score 74; DB 4; Length 109;
Best Local Similarity 83.3%; Pred. No. 0.0008;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 SSGTDFLTITSSLOAED 29
Db 66 SSGTDFLTITSSLOAED 83

RESULT 10
G9N0W5
ID 09N0W5 PRELIMINARY: PRT: 109 AA.
AC 09N0W5;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE ANTI-HUMAN A33 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE-20250927; PubMed-10788485;
RA Rader C., Ritzer G., Nathan S., Elia M., Gout I., Jungbluth A.A.,
RA Cohen L.S., Welt S., Old L.J., Barbas C.F. III.;
RT "The rabbit antibody repertoire as a novel source for the generation
RT of therapeutic human antibodies."
RT J. Biol. Chem. 275:13668-13676(2000).
DR EMBL: AF245502; AAF68449.1; -.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA: 11323 MW: BD8B396E75F94FB CRC64;

Query Match 50.7%; Score 73; DB 6; Length 109;
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Best Local Similarity 77.8%; Pred. No. 0.0011;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 12 SSGTDFLTITSSLOAED 29
Db 65 SSGTDFLTITSSLOAED 82

RESULT 11
ID 09UL74 PRELIMINARY: PRT: 99 AA.
AC 09UL74;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RX STRAIN-BALB/C;
RX MEDLINE-20448942; PubMed-10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RT Infect. Immun. 68:5803-5808(2000).
RL EMBL: AF206024; AAF69322.1; -.
FT NON_TER 99
FT NON_TER 99
SQ SEQUENCE 99 AA: 10939 MW: 3B25DE78453324 CRC64;

Query Match 49.3%; Score 71; DB 11; Length 99;
Best Local Similarity 77.8%; Pred. No. 0.0021;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 12 SSGTDFLTITSSLOAED 29
Db 57 SSGTDFLTITSSLOAED 74

RESULT 12
ID 09UL82 PRELIMINARY: PRT: 104 AA.
AC 09UL82;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
RX STRAIN-BALB/C;
RX MEDLINE-20448942; PubMed-10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RT Infect. Immun. 68:5803-5808(2000).
RL EMBL: AF206024; AAF69322.1; -.
FT NON_TER 99
FT NON_TER 99
SQ SEQUENCE 99 AA: 10939 MW: 3B25DE78453324 CRC64;
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DR HSSP; P01607; 1REI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_V.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 11360 MW; 5DA8BBED5F0AA1AE CRC64;

Query Match 48.6%; Score 70; DB 11; Length 104;
Best Local Similarity 77.8%; Pred. No. 0.0032;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 12 SSGCTDFTLTISLQAD 29
Db 62 SSGCTDFTLTISRVEAD 79

RESULT 13

ID Q9UL80 PRELIMINARY; PRT; 114 AA.

AC Q9UL80;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; Pubmed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berner S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035034; AAD56270.1; -
DR HSSP; P80362; IMTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 48.6%; Score 70; DB 4; Length 114;
Best Local Similarity 77.8%; Pred. No. 0.0035;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 12 SSGCTDFTLTISLQAD 29
Db 70 SSGCTDFTLTISRVEAD 87

RESULT 14

ID Q99M37 PRELIMINARY; PRT; 238 AA.

AC Q99M37;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHEICAL 26.3 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
RC TISSUE;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002035; AAH02035.1; -
DR HSSP; P01679; 2FBJ.
DR InterPro: IPR003597; Ig.
DR InterPro: IPR003597; Ig.
DR InterPro: IPR003600; Ig_C1.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_V.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00410; IGV_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
RW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 48.6%; Score 70; DB 11; Length 238;
Best Local Similarity 77.8%; Pred. No. 0.0079;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 12 SSGCTDFTLTISLQAD 29
Db 89 SSGCTDFTLTISRVEAD 106

RESULT 15

ID Q91WS9 PRELIMINARY; PRT; 233 AA.

AC Q91WS9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHEICAL 25.8 KDA PROTEIN (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AAH13496.1; -
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 47.9%; Score 69; DB 11; Length 233;
Best Local Similarity 72.2%; Pred. No. 0.011;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 12 SSGCTDFTLTISLQAD 29
Db 84 SSGCTDFTLTISLQAD 101

Search completed: July 15, 2002, 13:22:48
Job time: 1484 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 12:57:59 ; Search time 228.39 Seconds

(without alignments)
14.104 Million cell updates/sec

Title: US-09-712-819A-9

Perfect score: 144

Sequence: 1 YERKKRRQRRSGSGTDTFTLTISLQAFD 29

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: A_Geneseq_032802.*
2: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
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9: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
10: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
11: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
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18: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	60.4	82	19	AAW62807
2	87	60.4	94	19	AAW62808
3	87	60.4	107	20	AAW5269
4	87	60.4	111	15	AAW52059
5	87	60.4	112	18	AAW27527
6	87	60.4	113	15	AAW50313
7	87	60.4	113	15	AAW50314
8	87	60.4	113	17	AAW6489
9	87	60.4	113	19	AAW42466
10	87	60.4	113	21	AAW18857
11	87	60.4	113	21	AAW18861

12	87	60.4	113	21	AAW18863	Amino acid sequenc
13	87	60.4	113	21	AAW18869	Amino acid sequenc
14	87	60.4	113	21	AAW18871	Amino acid sequenc
15	87	60.4	113	21	AAW18873	Amino acid sequenc
16	87	60.4	113	21	AAW18879	Amino acid sequenc
17	87	60.4	113	21	AAW18881	Amino acid sequenc
18	87	60.4	113	22	AAW62769	Human H1V-1 monoclon
19	87	60.4	114	14	AAW30144	MAB G4H variable F
20	87	60.4	114	15	AAW45605	Monoclonal antibod
21	87	60.4	114	18	AAW15537	Anti-TGF beta-1 sc
22	87	60.4	115	15	AAW27546	Human Ab light cha
23	87	60.4	120	22	AAW61240	Monoclonal antibod
24	87	60.4	120	22	AAW65565	Amino acid sequenc
25	87	60.4	124	20	AAW57181	Amino acid sequenc
26	87	60.4	126	22	AAW77598	Anti-human VEGF re
27	87	60.4	126	22	AAW78867	Anti-human VEGF re
28	87	60.4	127	17	AAW06443	HumC3 VL region.
29	87	60.4	131	16	AAW75355	Humanized antibody
30	87	60.4	131	16	AAW70202	Humanized antibody
31	87	60.4	131	20	AAW23779	Light chain variab
32	87	60.4	131	20	AAW23771	Light chain variab
33	87	60.4	131	20	AAW18126	Light chain sequen
34	87	60.4	131	20	AAW18118	Light chain sequen
35	87	60.4	132	21	AAW07966	A light chain vari
36	87	60.4	133	9	AAW08894	V region of L chain
37	87	60.4	133	18	AAW21934	Variable light sub
38	87	60.4	133	20	AAW05264	Antibody 24-31 hum
39	87	60.4	134	20	AAW50690	Human Humd VL Clat
40	87	60.4	135	21	AAW03714	Immunoglobulin kap
41	87	60.4	137	18	AAW10547	Wild type murine a
42	87	60.4	137	18	AAW10544	Humanised murine a
43	87	60.4	137	18	AAW10545	Humanised murine a
44	87	60.4	147	20	AAW34314	IgM antibody CEM 1
45	87	60.4	149	20	AAW34311	IgM antibody CEM 1

ALIGNMENTS

RESULT	ID	Description
1	AAW62807	standard; peptide; 82 AA.
2	AAW62807	23-SEP-1998 (first entry)
3	AAW62807	Amino acid sequence of a human antibody fragment.
4	AAW62807	Human: immunoglobulin; Ig; transgenic; non-human mammal;
5	AAW62807	Inactivated endogenous Ig locus; B-cell development;
6	AAW62807	human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
7	AAW62807	kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
8	AAW62807	production; antibody.
9	AAW62807	Homo sapiens.
10	AAW62807	WO9824893-A2.
11	AAW62807	11-JUN-1998.
12	AAW62807	03-DEC-1997; 97WO-US23091.
13	AAW62807	03-DEC-1996; 96US-0759620.
14	AAW62807	(ABGE-) ABGENIX INC.
15	AAW62807	Green L, Jakobovits A, Klapholz S, Kucherlapati R;
16	AAW62807	Mendez M;
17	AAW62807	WPI; 1998-333314/29.
18	AAW62807	New transgenic non-human mammals - having an inactivated

XX This sequence is the variable light chain of a humanised antibody of
 CC the invention. The antibody is capable of competing with a murine 24-31
 CC antibody for inhibiting CD40 binding to gp39. The humanised antibodies
 CC can be used for the treatment of a disease treatable by modulating gp39
 CC expression or inhibiting the gp39/CD40 interaction. They can be used for
 CC treating e.g. autoimmune diseases such as rheumatoid arthritis, psoriasis
 CC multiple sclerosis, diabetes, systemic lupus erythematosus and idiopathic
 CC thrombocytopenic purpura (ITP) or non-autoimmune conditions such as
 CC graft-versus-host disease (GVHD) or graft rejection. They can also be
 CC used for the treatment of reversible obstructive airways disease,
 CC intestinal inflammations and allergies (e.g. coeliac disease, Crohn's
 CC disease and ulcerative colitis) and food-related allergies (e.g.
 CC migraine, rhinitis and eczema), transplant rejection, asthma, leukaemia,
 CC or lymphoma. The antibodies can also be used as immunosuppressants, in
 CC particular during gene or cellular therapy. They may be used to inhibit
 CC humoral and cellular immune responses against viral vectors, e.g.
 CC retroviral vectors or adenoviral vectors. The use of such antibodies
 CC should enable such cells or vectors to be administered repeatedly, which
 CC will facilitate treatment of chronic diseases such as cancers and
 CC autoimmune diseases.

XX Sequence 107 AA;

Query Match 60.4%; Score 87; DB 20; Length 107;
 Best Local Similarity 100.0%; Pred. No. 7.4e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSTDFTLTSSIQARD 29
 |||||
 Db 65 ssgsdtfltlssiqard 82

RESULT 4
 AAR52059

ID AAR52059 standard; Protein; 111 AA.

XX AAR52059;

DT 10-OCT-1996 (first entry)

XX Light chain variable region of human KV4B antibody.

XX antibody: humanised; murine: human; heavy chain: light; variable:
 KW framework region; complementarity determining region; reshaping;
 KM modelling; surface residue; modify.

XX Homo sapiens.

XX Key location/Qualifiers

FT 1..23 /label= framework_region_1

FT /note= "FR 1"

FT 24..40 /label= complementarity_determining_region_1

FT /note= "CDR 1"

FT 41..55 /note= "FR 2"

FT 56..62 /note= "CDR 2"

FT 63..95 /note= "FR 3"

FT /note= "CDR 3"

FT Region

EP592106-A1.

XX 13-APR-1994.

XX 07-SEP-1993; 93EP-0307051.

XX 09-SEP-1992; 92US-0942245.

XX (PEDE/) PEDERSEN J T.
 PA (IMMU-) IMMUNOGEN INC.

PI Guld BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;

DR WPI; 1994-120230/15.

PT Method of resurfacing of rodent antibodies to produce humanised
 PT antibody forms - for producing non-human antibodies with improved
 PT therapeutic efficiency by presenting human surface on V-region

XX Example 1; Fig 4A; 230pp; English.

XX Modification of a rodent antibody (Ab) or fragment by resurfacing in
 CC order to produce a humanised rodent Ab can be determined by calculating
 CC homology between murine and human Ab antibody surfaces. In order to test
 CC the resurfacing approach of the invention, three humanisation
 CC experiments were set up: (1) traditional loop grafting; (2) resurfacing
 CC approach using most similar chain; and (3) resurfacing approach using
 CC human sequences with most similar surface residues. The Ab used was the
 CC murine anti-N901 Ab (see AAR52055). Experiment 3 was carried out using
 CC the present sequence which represents the human KV4B Ab light chain
 CC variable region with 71 percent homology with anti-N901 Ab. N901/KV4B
 CC (AAR52060) was prepd. by resurfacing.

XX Sequence 111 AA;

Query Match 60.4%; Score 87; DB 15; Length 111;
 Best Local Similarity 100.0%; Pred. No. 7.7e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSTDFTLTSSIQARD 29
 |||||
 Db 70 ssgsdtfltlssiqard 87

RESULT 5
 AAM27527

ID AAM27527 standard; Protein; 112 AA.

XX AAM27527;

DT 16-DEC-1997 (first entry)

XX Light chain variable region of human CRA2 antibody.

XX Complementarity determining region; CDR; murine: mouse; human:
 KW high affinity; immunoglobulin B; receptor; monoclonal antibody;
 KW IGE; MA5; light chain; variable region; humanised; semi-chimeric;
 KM chimeric; treatment; prevention; disease; allergy; CRA2.

XX Homo sapiens.

XX JP09191886-A.

XX 29-JUL-1997.

XX 19-JAN-1996; 96JP-0024816.

XX 19-JAN-1996; 96JP-0024816.

XX (ASAK) ASAKI BREWERIES LTD.

XX (NIKK-) NIKKA WHISKEY KK.

XX (TORI) TORI YAKUHIN KK.

XX (TSUR/) TSURA T.

XX WPI; 1997-429186/40.

XX Humanised, semi-chimeric and chimeric antibodies against human
 PT high-affinity IGE receptor - useful medicinally and have low
 PT antigenicity in humans

XX Claim 2; Page 14; 26pp; Japanese.
 XX
 CC The present sequence, the light chain variable region of the human
 CC antibody (Ab) CRA2, was used in the preparation of a humanised or
 CC semi-chimeric monoclonal Ab (MAb), comprising complementarity
 CC determining regions (CDR) from a murine, anti-human high affinity
 CC immunoglobulin E (IgE) receptor, MAb. The humanised, semi-chimeric
 CC or chimeric MAb can be used to treat or prevent diseases,
 CC specifically allergies, associated with the receptor, and has very
 CC low antigenicity in humans.
 CC
 XX Sequence 112 AA;
 SO
 Query Match 60.4%; Score 87; DB 18; Length 112;
 Best Local Similarity 100.0%; Pred. No. 7.8e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 12 SGSGTDFLTITISLQAE 29
 Db 69 sgsqtdftltisslqae 86
 RESULT 6
 AAR50313
 ID AAR50313 standard; Protein; 113 AA.
 XX
 AC AAR50313;
 XX
 DT 05-OCT-1994 (first entry)
 XX
 DE Humanised light chain variable region Pfhlcl-1.
 XX
 KW Monoclonal antibody; Plasmodium falciparum; CDR;
 KW complementarity determining region; fusion protein;
 KW murine; variable; light; heavy; chain; malaria.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 24..40
 FT /label= CDR1
 FT Region 56..62
 FT /label= CDR2
 FT Region 95..103
 FT /label= CDR3
 XX
 PN WO9405690-A.
 XX
 PD 17-MAR-1994.
 XX
 PF 08-SEP-1993; 93WO-US08435.
 XX
 PR 09-SEP-1992; 92US-0941654.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (USNA) US SEC OF NAVY.
 PA (USNA) US SEC OF NAVY.
 XX
 PI Charoenvit Y, Hoffman S, Hurle M, Rosenberg M;
 PI Sadoff JC, Sylvester DR, Gross MS;
 XX
 DR WPI: 1994-10115/12.
 DR N-PSDB; AAQ44827.
 XX
 PT New engineered antibodies and fusion proteins for preventing
 PT Plasmodium infection - contg. murine antibody CDR sequences, and
 PT corresp. nucleic acid, vectors and transformed cells
 XX
 PS Claim 5; Fig 2; 98pp; English.
 CC Naturally-occurring (AAQ44841-42) and synthetic (AAQ44825-28)

CC variable light chain and variable heavy chain sequences
 CC derived from murine mAb NPS2 are provided. Murine mAb NPS2,
 CC its variable chain peptides, CDRs, functional fragments,
 CC Fab fragments, and analogs are useful in prodn. of fusion
 CC proteins, esp. engineered antibodies. These prods. are
 CC used to protect humans against Plasmodium infections.
 CC
 XX Sequence 113 AA;
 SO
 Query Match 60.4%; Score 87; DB 15; Length 113;
 Best Local Similarity 100.0%; Pred. No. 7.8e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 12 SGSGTDFLTITISLQAE 29
 Db 71 sgsqtdftltisslqae 88
 RESULT 7
 AAR50314
 ID AAR50314 standard; Protein; 113 AA.
 XX
 AC AAR50314;
 XX
 DT 05-OCT-1994 (first entry)
 XX
 DE Humanised light chain variable region Pfhlcl-2.
 XX
 KW Monoclonal antibody; Plasmodium falciparum; CDR;
 KW complementarity determining region; fusion protein;
 KW murine; variable; light; heavy; chain; malaria.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 24..40
 FT /label= CDR1
 FT Region 56..62
 FT /label= CDR2
 FT Region 95..103
 FT /label= CDR3
 XX
 PN WO9405690-A.
 XX
 PD 17-MAR-1994.
 XX
 PF 08-SEP-1993; 93WO-US08435.
 XX
 PR 09-SEP-1992; 92US-0941654.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (USNA) US SEC OF NAVY.
 PA (USNA) US SEC OF NAVY.
 XX
 PI Charoenvit Y, Hoffman S, Hurle M, Rosenberg M;
 PI Sadoff JC, Sylvester DR, Gross MS;
 XX
 DR WPI: 1994-10115/12.
 DR N-PSDB; AAQ44828.
 XX
 PT New engineered antibodies and fusion proteins for preventing
 PT Plasmodium infection - contg. murine antibody CDR sequences, and
 PT corresp. nucleic acid, vectors and transformed cells
 XX
 PS Claim 5; Fig 3; 98pp; English.
 CC Naturally-occurring (AAQ44841-42) and synthetic (AAQ44825-28)
 CC variable light chain and variable heavy chain sequences
 CC derived from murine mAb NPS2 are provided. Murine mAb NPS2,
 CC its variable chain peptides, CDRs, functional fragments,
 CC Fab fragments, and analogs are useful in prodn. of fusion
 CC proteins, esp. engineered antibodies. These prods. are

PA	(SMIK) SMITHKLINE BEECHAM CORP.
XX	
PI	Appelbaum ER, Cook RM;
DR	WPI; 1998-062853/06.
DR	N-PSDB; AA03497.
XX	
PT	Use of neutralising antibody to human Interleukin-5 - that does not
PT	block binding to receptor alpha chain, to treat e.g. asthma,
PT	allergic rhinitis or atopic dermatitis
PS	
PS	Example 4; Fig 9; 116pp; English.
XX	
CC	This polypeptide comprises a humanised antibody light chain
CC	variable region composed of human LEN framework regions and
CC	complementarily determining regions (see AAW42460-62) derived from
CC	anti-human interleukin-5 (IL-5) murine monoclonal antibody (MAb)
CC	226 light chain (see AAW42452). It is encoded by a DNA construct
CC	(see AAV03497) in vector pCMT15H2LCL1.0 (see AAV03504). The humanised
CC	light chain has been expressed in transfected COS host cells. The
CC	invention provides antibodies, especially altered, chimeric and
CC	humanised antibodies which are characterised by IL-5 specificity,
CC	neutralising activity and affinity for IL-5. The antibodies are
CC	useful for treating IL-5-mediated disorders such as asthma,
CC	allergic rhinitis and atopic dermatitis, and can also be used in
CC	the diagnosis of such conditions by measurement (e.g. by ELISA) of
CC	endogenous IL-5 levels. Also provided are vectors and transformed
CC	host cells for expression of the novel antibodies.
SQ	
SQ	Sequence 113 AA:
Query Match	60.4%; Score 87; DB 19; Length 113;
Best Local Similarity	100.0%; Pred. No. 7 Be-05;
Matches 18; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	12 SGSGDTFTLRISLAQD 29
Db	71 SGGTDFLTLSIQAED 88
RESULT 10	
AAB18857	
ID	AAB18857 standard; Protein; 113 AA.
XX	
AC	AAB18857;
XX	
D7	08-FEB-2001 (first entry)
XX	
DE	Amino acid sequence of anti-p53 antibody light chain clone 163.2.
XX	
KM	p53; antibody; immune response; vaccine; gene therapy; cancer;
KM	rheumatoid arthritis; coronary heart disease.
OS	Homo sapiens.
XX	
PN	WO200056770-A1.
PD	
XX	28-SEP-2000.
XX	
PE	15-MAR-2000; 2000MC-AU00189.
XX	
PR	19-MAR-1999; 99AU-0009321.
XX	
PA	(SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
XX	
PI	Mard RL, Coomber DMJ;
XX	
DR	WPI: 2000-638249/61.
XX	
XX	N-PSDB; AAA96134.
XX	
PT	'polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
PT	fragments, useful in treatment and diagnosis of cancer, rheumatoid

PT arthritis and coronary heart disease -

XX
PS Claim 30; Page 132; 163pp; English.

CC The present sequence represents the light chain of an antibody reactive
CC against p53. The antibody is obtained from a vertebrate host expressing
CC an immune response against a naturally occurring disease. The antibodies
CC are useful in pharmaceutical compositions, which additionally contain
CC chelators, drugs, prodrugs, toxins and imaging markers e.g. radioisotopes
CC or gadolinium. The polypeptide components of the antibodies are useful in
CC vaccines, for inducing an immune response against a disease in a
CC vertebrate, for treatment and/or prophylaxis of disease and for detection
CC purposes. The nucleic acid sequences can be used to detect a disease as
CC well as for gene therapy and recombinant production of the polypeptides.
CC In particular, the following can be treated cancer, rheumatoid arthritis
CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

CC
CC Sequence 113 AA:

XX
SQ

Query Match 60.4%; Score 87; DB 21; Length 113;
Best Local Similarity 100.0%; Pred. No. 7 8e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SGSGDFTLTITSSIAED 29
|||||
Db 71 sgsydfdltlssiqaed 88

RESULT 11

ID AAB18861 standard; Protein; 113 AA.

XX
AC AAB18861;

XX
DT 08-FEB-2001 (First entry)

XX
DE Amino acid sequence of anti-p53 antibody light chain clone 163.6.

XX
KW p53; antibody; immune response; vaccine; gene therapy; cancer;
KW rheumatoid arthritis; coronary heart disease.

XX
OS Homo sapiens.

XX
PN W0200056770-A1.

XX
PD 28-SEP-2000.

XX
PE 15-MAR-2000; 2000MO-AU00189.

XX
PR 19-MAR-1999; 99AU-0009321.

XX
PA (SVIN-) ST VINCENT'S HOSPITAL, SYDNEY LTD.

XX
PI Ward RL, Coomber DMJ;

XX
DR WPI; 2000-638249/61.

XX
DR N-PSDB; AAA96138.

XX
PT polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
PT arthritis and coronary heart disease -

XX
PS Claim 30; Page 136; 163pp; English.

CC The present sequence represents the light chain of an antibody reactive
CC against p53. The antibody is obtained from a vertebrate host expressing
CC an immune response against a naturally occurring disease. The antibodies

are useful in pharmaceutical compositions, which additionally contain chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes or gadolinium. The polypeptide components of the antibodies are useful in vaccines, for inducing an immune response against a disease in a vertebrate, for treatment and/or prophylaxis of disease and for detection purposes. The nucleic acid sequences can be used to detect a disease as well as for gene therapy and recombinant production of the polypeptides. In particular, the following can be treated cancer, rheumatoid arthritis and coronary heart disease. Cancers include carcinogenic tumours, tumours of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer, head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer, gastric cancer, brain cancer, bladder cancer, prostate cancer and urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours, e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

Sequence 113 AA:

Query Match 60.4%; Score 87; DB 21; Length 113;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SGGSGDTFTLTSSLSQAED 29
|||||
DB 71 ssgsgdtftltsslsqaed 88

RESULT 12
AAB18863
ID AAB18863 standard; Protein; 113 AA.
XX
XX AAB18863;
XX
DT 08-FEB-2001 (first entry)
XX
DE Amino acid sequence of anti-p53 antibody light chain clone 163.7.
XX
XX p53; antibody; immune response; vaccine; gene therapy; cancer;
XX
XX Rheumatoid arthritis; coronary heart disease.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 101 /note= "Arg encoded by CCA"
XX
XX PN WO200056770-A1.
XX
XX 28-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-AU00189.
XX
XX 19-MAR-1999; 99AU-0009321.
XX
XX (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
XX
XX Ward RL, Coomber DMJ;
XX
XX WPI: 2000-638249/61.
XX
XX N-PSDB: AAA96140.
XX
XX Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide fragments, useful in treatment and diagnosis of cancer, rheumatoid arthritis and coronary heart disease -
XX
XX
XX Claim 30; Page 138; 163pp; English.
XX
XX The present sequence represents the light chain of an antibody reactive against p53. The antibody is obtained from a vertebrate host expressing an immune response against a naturally occurring disease. The antibodies are useful in pharmaceutical compositions, which additionally contain chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes or gadolinium. The polypeptide components of the antibodies are useful in

vaccines, for inducing an immune response against a disease in a vertebrate, for treatment and/or prophylaxis of disease and for detection purposes. The nucleic acid sequences can be used to detect a disease as well as for gene therapy and recombinant production of the polypeptides. In particular, the following can be treated cancer, rheumatoid arthritis and coronary heart disease. Cancers include carcinogenic tumours, tumours of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer, head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer, gastric cancer, brain cancer, bladder cancer, prostate cancer and urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours, e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

Sequence 113 AA:

Query Match 60.4%; Score 87; DB 21; Length 113;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SGGSGDTFTLTSSLSQAED 29
|||||
DB 71 ssgsgdtftltsslsqaed 88

RESULT 13
AAB18869
ID AAB18869 standard; Protein; 113 AA.
XX
XX AAB18869;
XX
DT 08-FEB-2001 (first entry)
XX
DE Amino acid sequence of anti-p53 antibody light chain clone 163.15.
XX
XX p53; antibody; immune response; vaccine; gene therapy; cancer;
XX
XX Rheumatoid arthritis; coronary heart disease.
XX
XX Homo sapiens.
XX
XX PN WO200056770-A1.
XX
XX 28-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-AU00189.
XX
XX 19-MAR-1999; 99AU-0009321.
XX
XX (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
XX
XX Ward RL, Coomber DMJ;
XX
XX WPI: 2000-638249/61.
XX
XX N-PSDB: AAA96146.
XX
XX Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide fragments, useful in treatment and diagnosis of cancer, rheumatoid arthritis and coronary heart disease -
XX
XX
XX Claim 30; Page 144; 163pp; English.
XX
XX The present sequence represents the light chain of an antibody reactive against p53. The antibody is obtained from a vertebrate host expressing an immune response against a naturally occurring disease. The antibodies are useful in pharmaceutical compositions, which additionally contain chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes or gadolinium. The polypeptide components of the antibodies are useful in vaccines, for inducing an immune response against a disease in a vertebrate, for treatment and/or prophylaxis of disease and for detection purposes. The nucleic acid sequences can be used to detect a disease as well as for gene therapy and recombinant production of the polypeptides. In particular, the following can be treated cancer, rheumatoid arthritis and coronary heart disease. Cancers include carcinogenic tumours, tumours of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,

CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.
XX
SQ Sequence 113 AA;

Query Match 60.4%; Score 87; DB 21; Length 113;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SGGCTDFTLTITSSQAED 29
|||||
DB 71 sgsygdftltisslgaed 88

RESULT 14

AAB18871
ID AAB18871 standard; Protein; 113 AA.

XX
AC AAB18871;

DT 08-FEB-2001 (first entry)

XX Amino acid sequence of anti-p53 antibody light chain clone 163.16.

XX p53; antibody; immune response; vaccine; gene therapy; cancer;

KM rheumatoid arthritis; coronary heart disease.

OS Homo sapiens.

XX MO200056770-A1.

XX 28-SEP-2000.

XX 15-MAR-2000; 2000MO-AU00189.

XX 19-MAR-1999; 99AU-0009321.

XX (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.

PI Ward RL, Coomber DMJ;

XX WPI: 2000-638249/61.

DR N-PSDB; AAA96148.

XX Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
PT arthritis and coronary heart disease -

XX Claim 30; Page 146; 163pp; English.

CC The present sequence represents the light chain of an antibody reactive
CC against p53. The antibody is obtained from a vertebrate host expressing
CC an immune response against a naturally occurring disease. The antibodies
CC are useful in pharmaceutical compositions, which additionally contain
CC chelators, drugs, prodrgs, toxins and imaging markers e.g. radioisotopes
CC or gadolinium. The polypeptide components of the antibodies are useful in
CC vaccines, for inducing an immune response against a disease in a
CC vertebrate, for treatment and/or prophylaxis of disease and for detection
CC purposes. The nucleic acid sequences can be used to detect a disease as
CC well as for gene therapy and recombinant production of the polypeptides.
CC In particular, the following can be treated cancer, rheumatoid arthritis
CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

XX Sequence 113 AA;

SO

Query Match 60.4%; Score 87; DB 21; Length 113;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SGGCTDFTLTITSSQAED 29
|||||
DB 71 sgsygdftltisslgaed 88

RESULT 15

AAB18873
ID AAB18873 standard; Protein; 113 AA.

XX
AC AAB18873;

DT 08-FEB-2001 (first entry)

XX Amino acid sequence of anti-p53 antibody light chain clone 163.17.

XX p53; antibody; immune response; vaccine; gene therapy; cancer;

KM rheumatoid arthritis; coronary heart disease.

OS Homo sapiens.

XX MO200056770-A1.

XX 28-SEP-2000.

XX 15-MAR-2000; 2000MO-AU00189.

XX 19-MAR-1999; 99AU-0009321.

XX (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.

PI Ward RL, Coomber DMJ;

XX WPI: 2000-638249/61.

DR N-PSDB; AAA96150.

XX Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
PT arthritis and coronary heart disease -

XX Claim 30; Page 148; 163pp; English.

CC The present sequence represents the light chain of an antibody reactive
CC against p53. The antibody is obtained from a vertebrate host expressing
CC an immune response against a naturally occurring disease. The antibodies
CC are useful in pharmaceutical compositions, which additionally contain
CC chelators, drugs, prodrgs, toxins and imaging markers e.g. radioisotopes
CC or gadolinium. The polypeptide components of the antibodies are useful in
CC vaccines, for inducing an immune response against a disease in a
CC vertebrate, for treatment and/or prophylaxis of disease and for detection
CC purposes. The nucleic acid sequences can be used to detect a disease as
CC well as for gene therapy and recombinant production of the polypeptides.
CC In particular, the following can be treated cancer, rheumatoid arthritis
CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

XX Sequence 113 AA;

SO

Query Match 60.4%; Score 87; DB 21; Length 113;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SGGCTDFTLTITSSQAED 29
|||||

Db 71 ssgtdftltssiqaed 88

Search completed: July 15, 2002, 12:57:59
Job time: 415 sec

1
2
3

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2002, 12:59:20 ; Search time 75.67 seconds
(without alignments)
9.361 Million cell updates/sec

Title: US-09-712-819A-9

Percent score: 144
Sequence: 1 YERRRRRRSGSGTDFLTITSLQAE D 29

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents, AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PTUG.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/Backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	60.4	80	3	US-08-554-840-13
2	87	60.4	80	3	US-08-554-840-15
3	87	60.4	107	3	US-08-554-840-2
4	87	60.4	107	4	US-08-525-539A-81
5	87	60.4	112	1	US-07-942-245-30
6	87	60.4	113	1	US-08-467-420A-21
7	87	60.4	113	1	US-08-470-110A-21
8	87	60.4	113	1	US-08-667-769A-21
9	87	60.4	113	2	US-08-940-371-21
10	87	60.4	113	3	US-08-637-647-21
11	87	60.4	113	4	US-08-525-539A-80
12	87	60.4	113	5	PCT-US93-08435-6
13	87	60.4	113	5	PCT-US93-08435-8
14	87	60.4	113	5	PCT-US95-17082A-21
15	87	60.4	114	1	US-08-360-125-6
16	87	60.4	114	1	US-08-450-578-6
17	87	60.4	114	2	US-09-017-628-6
18	87	60.4	114	2	US-09-014-880-6
19	87	60.4	114	4	US-09-025-769B-17
20	87	60.4	115	4	US-09-025-769B-31
21	87	60.4	115	4	US-09-025-769B-49
22	87	60.4	120	1	US-08-025-320A-4
23	87	60.4	127	4	US-08-525-539A-65
24	87	60.4	131	2	US-08-483-636-14
25	87	60.4	131	2	US-08-483-636-58
26	87	60.4	131	2	US-08-483-632-14
27	87	60.4	131	2	US-08-483-632-58

28	87	60.4	133	3	US-08-463-903-4	Sequence 4, Appl
29	87	60.4	133	4	US-07-935-695-4	Sequence 4, Appl
30	87	60.4	135	3	US-08-812-586-46	Sequence 46, Appl
31	87	60.4	155	3	US-08-828-741B-11	Sequence 11, Appl
32	87	60.4	155	4	US-09-160-567-11	Sequence 11, Appl
33	87	60.4	171	3	US-08-463-903-20	Sequence 20, Appl
34	87	60.4	171	4	US-07-935-695-20	Sequence 20, Appl
35	87	60.4	241	2	US-07-916-098A-56	Sequence 56, Appl
36	87	60.4	260	3	US-08-463-903-2	Sequence 2, Appl
37	87	60.4	260	4	US-07-935-695-2	Sequence 2, Appl
38	87	60.4	275	3	US-08-463-903-6	Sequence 6, Appl
39	87	60.4	275	4	US-07-935-695-6	Sequence 6, Appl
40	87	60.4	285	3	US-08-463-903-22	Sequence 22, Appl
41	87	60.4	285	4	US-07-935-695-22	Sequence 22, Appl
42	87	60.4	342	3	US-08-828-741B-6	Sequence 6, Appl
43	87	60.4	342	4	US-09-160-567-6	Sequence 6, Appl
44	87	60.4	495	3	US-08-828-741B-4	Sequence 4, Appl
45	87	60.4	495	4	US-09-160-567-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-554-840-13
Sequence 13, Application US/08554840
Patent No. 6001358
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabli
APPLICANT: PADLAN, Eduardo A.
APPLICANT: NEWMAN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
TITILE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-554-840-13

Query Match 60.4%, Score 87, DB 3, Length 80;
Best Local Similarity 100.0%, Pred. No. 1,le-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 SGSGTDFLTITSLQAE D 29

Db 47 SGGSDPTLTITSSIAQED 64

```
|||||
RESULT 2
US-08-554-840-15
; Sequence 15, Application US/08554840
; Patent No. 6001358
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,840
; FILING DATE: 07-NOV-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-554-840-15

Query Match 60.4%; Score 87; DB 3; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SGGSDPTLTITSSIAQED 29
Db 47 SGGSDPTLTITSSIAQED 64

RESULT 3
US-08-554-840-2
; Sequence 2, Application US/08554840
; Patent No. 6001358
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEWMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
```

```
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,840
; FILING DATE: 07-NOV-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-554-840-2
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Query Match 60.4%; Score 87; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SGGSDPTLTITSSIAQED 29
Db 65 SGGSDPTLTITSSIAQED 82

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RESULT 4
US-08-525-539A-81
; Sequence 81, Application US/08525539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO GOUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
```

TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-525-539A-81

Query Match 60.4%; Score 87; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 SGSGTDFLTITSSLOAED 29
|||||

RESULT 5
US-07-942-245-30
Sequence 30, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSEE: Suphrine, Mon, 21nn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Morstation
OPERATING SYSTEM: UNIX
SOFTWARE: in house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942.245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-30

Query Match 60.4%; Score 87; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 SGSGTDFLTITSSLOAED 29
|||||

RESULT 6
US-08-467-420A-21

Sequence 21, Application US/08467420A
Patent No. 5683892
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful In
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P. O. Box 1559-0W2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,420A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5024
TELEFAX: 610 270-5090
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-420A-21

Query Match 60.4%; Score 87; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 SGSGTDFLTITSSLOAED 29
|||||

RESULT 7
US-08-470-110A-21
Sequence 21, Application US/08470110A
Patent No. 5693323
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.

;; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
;; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
;; NUMBER OF SEQUENCES: 74
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SmithKline Beecham Corp./Corporate
;; ADDRESSEE: Intellectual Property
;; STREET: P. O. Box 1539-UM2220
;; CITY: King of Prussia
;; STATE: Pennsylvania
;; COUNTRY: USA
;; ZIP: 19406-0939
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; FILING DATE: 06-JUN-1995
;; APPLICATION NUMBER: US 08/467420
;;
;; PRIORITY APPLICATION DATA:
;; FILING DATE: 23-DEC-1994
;; APPLICATION NUMBER: US 08/363131
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sulton, Jeffrey A.
;; REGISTRATION NUMBER: 34,028
;; REFERENCE/DOCKET NUMBER: P50282
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610 270-5024
;; TELEFAX: 610 270-5090
;;
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 113 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
;; US-08-470-110a-21

Query Match 60.4%; Score 87; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SGGCTDFTLTITSSLOAED 29
Db 71 SGGCTDFTLTITSSLOAED 88

RESULT 8
US-08-667-769a-21
; Sequence 21, Application US/08667769a
; Patent No. 5783184
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; STREET: P.O. Box 1539-UM2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/667,769a
;; FILING DATE:
;; CLASSIFICATION: 426
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/17082
;; FILING DATE: 22-DEC-1995
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/470110
;; FILING DATE: 06-JUN-1995
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/467420
;; FILING DATE: 06-JUN-1995
;;
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/363131
;; FILING DATE: 23-DEC-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sulton, Jeffrey A.
;; REGISTRATION NUMBER: 34,028
;; REFERENCE/DOCKET NUMBER: P50503
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-270-5024
;; TELEFAX: 610-270-5090
;;
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 113 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
;; US-08-667-769a-21

Query Match 60.4%; Score 87; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SGGCTDFTLTITSSLOAED 29
Db 71 SGGCTDFTLTITSSLOAED 88

RESULT 9
US-08-940-371-21
; Sequence 21, Application US/08940371
; Patent No. 5851525
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; STREET: P. O. Box 1539-UM2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,371
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/470,110
FILING DATE:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5024
TELEFAX: 610 270-5090
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-940-371-21

Query Match 60.4%; Score 87; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSTDFLTITSSLOAED 29
|||||
DB 71 SSGSTDFLTITSSLOAED 88

RESULT 10
US-08-637-647-21
Sequence 21, Application US/08637647
Patent No. 6129913
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TREATMENT OF ALLERGIC DISORDERS
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smitline Beecham Corp./Corporate
ADDRESS: Intellectual Property
STREET: P. O. Box 1539-0W2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,647
FILING DATE: 19-JUN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/363,131
FILING DATE:
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5024
TELEFAX: 610 270-5090
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-637-647-21

Query Match 60.4%; Score 87; DB 3; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 SSGSTDFLTITSSLOAED 29
|||||
DB 71 SSGSTDFLTITSSLOAED 88

RESULT 11
US-08-525-539A-80
Sequence 80, Application US/08525539A
Patent No. 6309636
GENERAL INFORMATION:
APPLICANT: DO COUTO, FERNANDO J.R.
APPLICANT: CERIANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & ROEBSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-525-539A-80

Query Match 60.4%; Score 87; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 12 SGSGTDFLTITSSLOAED 29
|
Db 71 SGSGTDFLTITSSLOAED 88

RESULT 12

PCT-US93-08435-6
Sequence 6, Application PC/TUS9308435
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
TITLE OF INVENTION: Novel Antibodies for Confering Passive
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 Norristown Road
CITY: Spring House
STATE: PA
COUNTRY: USA
ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: SBC P50107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-08435-6

Query Match 60.4%; Score 87; DB 5; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 12 SGSGTDFLTITSSLOAED 29
|
Db 71 SGSGTDFLTITSSLOAED 88

RESULT 13

PCT-US93-08435-8
Sequence 8, Application PC/TUS9308435
GENERAL INFORMATION:

APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Army
TITLE OF INVENTION: Novel Antibodies for Confering Passive

TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Box 457, 321 Norristown Road
CITY: Spring House
STATE: PA
COUNTRY: USA
ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08435
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/941,654
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: SBC P50107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9200
TELEFAX: (215) 540-5818

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-08435-8

Query Match 60.4%; Score 87; DB 5; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 12 SGSGTDFLTITSSLOAED 29
|
Db 71 SGSGTDFLTITSSLOAED 88

RESULT 14

PCT-US93-17082A-21
Sequence 21, Application PC/TUS9517082A
GENERAL INFORMATION:

APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard W.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
STREET: P.O. Box 1539-0W2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/17082A
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/470110
;; FILING DATE: 06-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/467420
;; FILING DATE: 06-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/363131
;; FILING DATE: 23-DEC-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sutton, Jeffrey A.
;; REGISTRATION NUMBER: 34,028
;; REFERENCE/DOCKET NUMBER: P50282-2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-270-5024
;; TELEFAX: 610-270-5090
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 113 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; PCT-US95-17082a-21

Query Match 60.4%; Score 87; DB 5; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SSGSGDTFTLTSSLAQAD 29
|||||
DB 71 SSGSGDTFTLTSSLAQAD 88

RESULT 15
US-08-360-125-6
; Sequence 6, Application US/08360125
; Patent No. 5767246
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki YAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: No. 5767246hiko ITO
; APPLICANT: Kazuhiko NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,125
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; APPLICATION NUMBER:

;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warren M. Cheek, Jr.
;; REGISTRATION NUMBER: 33,367
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-8850
;; TELEFAX:
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 114 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHEICAL:
;; ANTI-SENSE:
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE: Hybridoma producing human
;; CELL TYPE: antibody GAH
;; ORGANELLE:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURE:
;; NAME/KEY:
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-6

Query Match 60.4%; Score 87; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SSGSGDTFTLTSSLAQAD 29
|||||
DB 71 SSGSGDTFTLTSSLAQAD 88

Search completed: July 15, 2002, 12:59:20
Job time: 391 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 13:01:03 ; Search time 95.45 seconds
(without alignments)
29.194 Million cell updates/sec

Title: US-09-712-819A-10

Perfect score: 144
Sequence: 1 YEKRRRORRRSGTDATAPASSLOAED 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	63	43.8	92	2	S37533 Ig kappa chain V r
2	63	43.8	92	2	S37530 Ig kappa chain V r
3	63	43.8	92	2	S37529 Ig kappa chain V r
4	63	43.8	92	2	S37535 Ig kappa chain V r
5	63	43.8	92	2	S37531 Ig kappa chain V r
6	63	43.8	92	2	S37534 Ig kappa chain V r
7	63	43.8	92	2	S37532 Ig kappa chain V r
8	63	43.8	101	2	PH0869 Ig kappa chain V r
9	63	43.8	102	2	B34153 Ig kappa chain V r
10	63	43.8	106	2	A49138 Ig kappa chain V-I
11	63	43.8	113	2	S30523 Ig kappa chain V r
12	63	43.8	113	2	S30520 Ig kappa chain V r
13	63	43.8	113	2	S34003 Ig kappa chain V r
14	63	43.8	113	2	S34002 Ig kappa chain V r
15	63	43.8	114	1	K4HUN1 Ig kappa chain V-I
16	63	43.8	114	2	S44116 Ig kappa chain V-I
17	63	43.8	120	1	S51147 antibody light cha
18	63	43.8	121	1	K4HUN1 Ig kappa chain pre
19	63	43.8	124	1	S40364 Ig kappa chain - h
20	63	43.8	133	1	K4HUN1 Ig kappa chain pre
21	63	43.8	134	1	K4HUN1 Ig kappa chain pre
22	63	43.8	134	1	S49531 anti-5m antibody V
23	63	42.4	105	2	C30535 Ig kappa chain V r
24	61	42.4	113	2	JC3270 p27-6 antibody lig
25	60	41.7	79	2	S24215 Ig kappa chain - m
26	60	41.7	81	2	PH1048 Ig kappa chain V r
27	60	41.7	97	2	A42575 Ig kappa chain V r
28	60	41.7	101	2	S26337 Ig light chain V r
29	60	41.7	101	2	PH1046 Ig light chain V r

30	60	41.7	102	2	A34153 Ig kappa chain V-I
31	60	41.7	103	2	PH1050 Ig light chain V r
32	60	41.7	103	2	PH1051 Ig light chain V r
33	60	41.7	103	2	PH1052 Ig light chain V r
34	60	41.7	103	2	PH1054 Ig light chain V r
35	60	41.7	103	2	PH1047 Ig light chain V r
36	60	41.7	104	2	PH1053 Ig light chain V r
37	60	41.7	104	2	PH1101 Ig light chain V r
38	60	41.7	104	2	PH1102 Ig light chain V r
39	60	41.7	104	2	PH1103 Ig light chain V r
40	60	41.7	104	2	PH1104 Ig light chain V r
41	60	41.7	104	2	C30534 Ig kappa chain V r
42	60	41.7	105	2	A30534 Ig kappa chain V r
43	60	41.7	107	2	B30535 Ig kappa chain V r
44	60	41.7	107	2	G30535 Ig kappa chain V r
45	60	41.7	107	2	D30535 Ig kappa chain V r

ALIGNMENTS

RESULT 1
S37533
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37533
R:Klein, U.; Kuipers, R.; Rajewsky, K.
Submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)19D(+) cells, the major B cell subset in the peripheral bl
A:Reference number: S37530
A:Accession: S37533
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:226627, NID:9405708, PIDN:CAA81380.1; PID:9405709
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 43.8%; Score 63; DB 2; Length 92;
Best Local Similarity 77.8%; Pred. No. 0.31;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGGTDATAPASSLOAED 29
Db 49 SSGGTDFTLTSSLOAED 66

RESULT 2
S37530
Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37530
R:Klein, U.; Kuipers, R.; Rajewsky, K.
Submitted to the EMBL Data Library, September 1993
A:Description: Human IGM(+)19D(+) cells, the major B cell subset in the peripheral bl
A:Reference number: S37501
A:Accession: S37530
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:226630, NID:9405702, PIDN:CAA81383.1; PID:9405703
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 43.8%; Score 63; DB 2; Length 92;
Best Local Similarity 77.8%; Pred. No. 0.31;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 12 SSGGTDATAPASSLOAED 29

Db 49 SSGSDFTLTISSLOAED 66

RESULT 3

Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37529
R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37529
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:226631; NID:g405700; PIDN:CAA81384.1; PID:g405701
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 43.8%; Score 63; DB 2; Length 92;
Best Local Similarity 77.8%; Pred. No. 0.31;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 12 SSGSDATAPASSLOAED 29
Db 49 SSGSDFTLTISSLOAED 66

RESULT 4

Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37535
R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37535
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:226625; NID:g405712; PIDN:CAA81378.1; PID:g405713
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 43.8%; Score 63; DB 2; Length 92;
Best Local Similarity 77.8%; Pred. No. 0.31;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 12 SSGSDATAPASSLOAED 29
Db 49 SSGSDFTLTISSLOAED 66

RESULT 5

Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37531
R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37531
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:226629; NID:g405704; PIDN:CAA81382.1; PID:g405705
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 43.8%; Score 63; DB 2; Length 92;
Best Local Similarity 77.8%; Pred. No. 0.31;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 12 SSGSDATAPASSLOAED 29
Db 49 SSGSDFTLTISSLOAED 66

RESULT 6

Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37534
R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37534
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:226626; NID:g405710; PIDN:CAA81379.1; PID:g405711
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 43.8%; Score 63; DB 2; Length 92;
Best Local Similarity 77.8%; Pred. No. 0.31;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 12 SSGSDATAPASSLOAED 29
Db 49 SSGSDFTLTISSLOAED 66

RESULT 7

Ig kappa chain V region (V-kappa 4) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37532
R:Klein, U.; Kuipers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A:Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A:Reference number: S37501
A:Accession: S37532
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <KLE>
A:Cross-references: EMBL:226628; NID:g405706; PIDN:CAA81381.1; PID:g405707
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 43.8%; Score 63; DB 2; Length 92;
Best Local Similarity 77.8%; Pred. No. 0.31;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 12 SSGSDATAPASSLOAED 29
Db 49 SSGSDFTLTISSLOAED 66

RESULT 8

PH0869

Ig kappa chain V region (anti-DNA, H2F) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C:Accession: PH0869
R:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghosssein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idotype
A:Reference number: PH0862; MUID:92078875
A:Accession: PH0869
A:Molecule type: DNA
A:Residues: 1-101 <MAN>
A>Note: residues 28-33 were obtained from Figure 4
C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-23/Region: framework 1
F:16-96/Domain: immunoglobulin homology <IMM>
F:24-40/Region: complementarity-determining 1
F:41-55/Region: complementarity-determining 2
F:56-62/Region: complementarity-determining 3
F:63-94/Region: framework 3
F:95-101/Region: complementarity-determining 3

Query Match 43.8%; Score 63; DB 2; Length 101;
Best Local Similarity 77.8%; Pred. No. 0.33;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGCTDATAPASSLQAE 29
DB 71 SSGCTDFTLTISLQAE 88

RESULT 9
B34153
Ig kappa chain V-IV region (Fue) - human
C:Species: Homo sapiens (man)
C:Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 21-Jan-2000
C:Accession: B34153
R:Milnesco, E.; Ayadi, H.; Conqy, N.; Gendron, M.C.; Roy, J.P.; Heyermann, H.; Frangione
J. Biol. Chem. 264, 21481-21485, 1989
A:Title: Multiple mutations in the variable region of the kappa light chains of three mc
A:Reference number: A34153; MUID:90094513
A:Accession: B34153
A:Molecule type: protein
A:Status: preliminary
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 43.8%; Score 63; DB 2; Length 102;
Best Local Similarity 77.8%; Pred. No. 0.34;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGCTDATAPASSLQAE 29
DB 71 SSGCTDFTLTISLQAE 88

RESULT 10
A49138
IgA kappa rheumatoid factor variable - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A49138
R:Gause, A.; Kupperts, R.; Mierau, R.
Clin. Exp. Immunol. 88, 430-434, 1992
A:Title: A somatically mutated V kappa IV gene encoding a human rheumatoid factor light
A:Reference number: A49138; MUID:92298590
A:Accession: A49138
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-106 <GAD>
A:Cross-references: GB:S37926; MID:q298207; PIDN:AAB22366.1; PID:9298208
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:106633, NCBI:106637)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:20-99/Domain: immunoglobulin homology <IMM>

Query Match 43.8%; Score 63; DB 2; Length 106;
Best Local Similarity 77.8%; Pred. No. 0.35;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGCTDATAPASSLQAE 29
DB 74 SSGCTDFTLTISLQAE 91

RESULT 11
S30523
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S30523
R:Marlette, X.
submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30523
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAR>
A:Cross-references: EMBL:218329
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 43.8%; Score 63; DB 2; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.37;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGCTDATAPASSLQAE 29
DB 71 SSGCTDFTLTISLQAE 88

RESULT 12
S30520
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S30520
R:Marlette, X.
submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30520
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAR>
A:Cross-references: EMBL:218325
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 43.8%; Score 63; DB 2; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.37;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGCTDATAPASSLQAE 29
DB 71 SSGCTDFTLTISLQAE 88

```

RESULT 13
S34003
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S34003
R:Marlette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A>Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A:Reference number: S34001; MUID:93209281
A:Accession: S34003
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAR>
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin
F:16-96/Domain: Immunoglobulin homology <IMM>

```

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Query Match 43.8%; Score 63; DB 2; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.37;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SGGCTDATAPASSIQAED 29
      ||||| | |||||
Db 71 SGGCTDFTLTISIQAED 88

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RESULT 14
S34002
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S34002; S30522
R:Marlette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A>Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A:Reference number: S34001; MUID:93209281
A:Accession: S34002
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAR>
A:Cross-references: EMBL:218328
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin
F:16-96/Domain: Immunoglobulin homology <IMM>

```

```

Query Match 43.8%; Score 63; DB 2; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.37;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SGGCTDATAPASSIQAED 29
      ||||| | |||||
Db 71 SGGCTDFTLTISIQAED 88

```

```

RESULT 15
K4HULN
Ig kappa chain V-IV region (Len) - human
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 01-Dec-2000
C:Accession: A01903; F61458
R:Schneider, M.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, 507-557, 1975
A>Title: Die Primerstruktur einer monoklonalen Immunoglobulin-L-Kette der Subgruppe IV
A:Reference number: A01903; MUID:76004342
A:Accession: A01903
A:Molecule type: protein
A:Residues: 1-114 <SCH>
A>Note: this is the first completely sequenced V region of a new kappa chain subgroup.
A>Note: the C region of this chain has the Inv (3) marker

```

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R:Brouet, J.C.; Dellagi, R.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Milnesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A>Title: Expression of a public Idiotypic by human monoclonal IgM directed to myelin-a
A:Reference number: A61458; MUID:90039128
A:Accession: F61458
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <BRD>
C:Comment: This is a Bence Jones protein.
C:Complex: An Immunoglobulin heterotrimer subunit consists of two identical light (
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin
F:16-96/Domain: Immunoglobulin homology <IMM>
F:23-94/Disulfide bonds: #status predicted

```

```

Query Match 43.8%; Score 63; DB 1; Length 114;
Best Local Similarity 77.8%; Pred. No. 0.37;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SGGCTDATAPASSIQAED 29
      ||||| | |||||
Db 71 SGGCTDFTLTISIQAED 88

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Search completed: July 15, 2002, 13:01:03
Job time: 469 sec


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AC P06312;
DT 01-JAN-1988 (Rel. 06, Created)
DT 15-JUN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region precursor (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Combratio G., Mocikat R., Pohlentz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene."
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -----
CC -I- MISCELLANEOUS: THERE IS ONLY ONE IG KAPPA V-IV GENE.
CC -----
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CC PIR; A01902; K4HU.
CC HSSP; P01789; IMCP.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >121 IG KAPPA CHAIN V-IV REGION.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DISULFD 43 114 BY SIMILARITY.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13380 MW; 9586AD4186D35974 CRC64;

Query Match 43.8%; Score 63; DB 1; Length 121;
Best Local Similarity 77.8%; Pred. No. 0.09;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGCTDATAAPASLOAED 29
DB 91 SSGCTDFTLITSSLOAED 108

RESULT 3
KVAB_HUMAN STANDARD; PRT; 133 AA.
ID P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Combratio G., Mocikat R., Pohlentz H.D.,

```

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RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene."
RL Nucleic Acids Res. 13:6515-6529(1985).
CC -----
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CC -----
CC EMBL; Z00022; CAAT7317.1; -.
CC PIR; A01904; K4HUJ1.
CC HSSP; P01789; IMCP.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 IG KAPPA CHAIN V-IV REGION JI.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING-3.
FT DISULFD 43 114 FRAMEWORK-4.
FT NON_TER 133 133 BY SIMILARITY.
SQ SEQUENCE 133 AA; 14632 MW; 5F83953066744AF4 CRC64;

Query Match 43.8%; Score 63; DB 1; Length 133;
Best Local Similarity 77.8%; Pred. No. 0.099;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGCTDATAAPASLOAED 29
DB 91 SSGCTDFTLITSSLOAED 108

RESULT 4
KVAC_HUMAN STANDARD; PRT; 134 AA.
ID P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned
RT cDNA probe."
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RA Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL: X02990; CA26733.1; -.
DR PIR: A01905; K4H07.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134
FT DOMAIN 21 43 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 133 FRAMEWORK-4.
FT DISUPTD 43 114 BY SIMILARITY.
FT NON_TER 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 43.8%; Score 63; DB 1; Length 134;
Best Local Similarity 77.8%; Pred. No. 0.1;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGSTDTAPASSLOAED 29
DB 91 SSGSTDEFTLTSSLOAED 108
||||| | |||||
12 SSGSTDTAPASSLOAED 29
12 SSGSTDEFTLTSSLOAED 108

RESULT 5
KV5A_MOUSE STANDARD; PRT; 149 AA.
AC P01633;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region MPCI1 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-71 FROM N.A.
RX MEDLINE=83001944; PubMed=6288267;
RA Kelley D.E., Coleclough C., Perry R.P.;
RT "Functional significance and evolutionary development of the
RT 5'-terminal regions of immunoglobulin variable-region genes.";
RL Cell 29:681-689(1982).
RN [2]
RP SEQUENCE OF 41-149 FROM N.A.
RX MEDLINE=80176554; PubMed=6245773;
RA Rabbits T.H., Hamlyn P.H., Matthysens G., Roe B.A.;
RT "The variability, arrangement, and rearrangement of immunoglobulin
RT genes.";
RL Can. J. Biochem. 58:176-187(1980).
RN [3]
RP SEQUENCE OF 30-149.
RX MEDLINE=78186617; PubMed=418775;
RA Smith G.P.;
RT "Sequence of the full-length immunoglobulin kappa-chain of mouse
RT myeloma MPC 11.";
RL Blochm. J. 171:337-347(1978).
CC -1- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT THE
CC AMINO END, DUE TO A TANDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE
CC CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL
CC RESIDUE OF TYPICAL KAPPA CHAINS.
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CC -----
DR EMBL: J00561; AAA38776.1; -.
DR PIR: A01916; KYMS11.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Signal; Repeat.
FT SIGNAL 1 29
FT CHAIN 30 149 IG KAPPA CHAIN V-V REGION MPCI1.
FT DOMAIN 42 64 FRAMEWORK-1.
FT DOMAIN 65 75 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 76 90 FRAMEWORK-2.
FT DOMAIN 91 97 FRAMEWORK-3.
FT DOMAIN 98 129 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 130 138 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 139 148 COMPLEMENTARITY-DETERMINING-4.
FT REPEAT 26 35
FT REPEAT 38 47
FT NON_TER 149
SQ SEQUENCE 149 AA; 16434 MW; B0480C87B662AC3E CRC64;

Query Match 41.0%; Score 59; DB 1; Length 149;
Best Local Similarity 72.2%; Pred. No. 0.38;
Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGSTDTAPASSLOAED 29
DB 106 SSGSTDEFTLTSSVQAED 123
||||| | |||||
12 SSGSTDTAPASSLOAED 29
106 SSGSTDEFTLTSSVQAED 123

RESULT 6
KV1H_HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau); subdivision within
RT subgroups.";
RL Hoppe-Sejler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
CC -----
DR PIR: A01868; K1HDH0.
DR HSSP: P80362; 1WTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT SIGNAL 1 23
FT CHAIN 24 149 FRAMEWORK-1.
FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 50 56 FRAMEWORK-2.
FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 89 97 FRAMEWORK-3.
FT DOMAIN 97 97 COMPLEMENTARITY-DETERMINING-3.
```

FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D00618 CRC64;

Query Match 40.3%; Score 58; DB 1; Length 108;
Best Local Similarity 72.2%; Pred. No. 0.36;

Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 12 SSGCTDATAPASSLOAED 29
Db 65 SSGCTDFTLTITSSLOPED 82

RESULT 7

KV3J_HUMAN STANDARD; PRT; 116 AA.

AC P04434;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-III region VH precursor (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC NCBI_TaxID=9606;

OX [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=85087932; PubMed=6440122;

RA Pech M., Zachau H.G.;

RT "Immunoglobulin genes of different subgroups are interdigitated

RT within the Vh locus.";

RL Nucleic Acids Res. 12:9229-9236(1984).

CC -----

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CC -----

CC EMBL: X02725; ; NOT_ANNOTATED_CDS.

DR PIR: A01901; K3HUVH.

DR HSSP: P01789; 2MCP.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_V.

DR Pfam: PF00047; Ig_V.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

RESULT 8
KV1L_HUMAN STANDARD; PRT; 117 AA.
AC P01601;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region HK101 precursor (Fragment).

Query Match 40.3%; Score 58; DB 1; Length 117;
Best Local Similarity 72.2%; Pred. No. 0.4;

Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 12 SSGCTDATAPASSLOAED 29
Db 87 SSGCTDFTLTITSSLOPED 104

RESULT 9

KV1W_HUMAN STANDARD; PRT; 129 AA.

AC P04431;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-I region VH precursor (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OC NCBI_TaxID=9606;

OX [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=81098966; PubMed=6779204;

RA Bentley D.L., Rabbits T.H.;

RT "Human immunoglobulin variable region genes -- DNA sequences of two V

RT kappa genes and a pseudogene.";

RL Nature 288:730-733(1980).

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CC -----

CC EMBL: K01322; AA58930.1; ;

DR EMBL: K01324; AA58932.1; ;

DR EMBL: V00558; CA23824.1; ;

DR PIR: A01881; K1H011.

DR PIR: A21056; A21056.

DR HSSP: P01607; 1REI.

DR InterPro: IPR003006; Ig_MHC.

DR InterPro: IPR003596; Ig_V.

DR Pfam: PF00047; Ig_V.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DR SMART: SM00406; IgV_1.

DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-1 region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=65014148; PubMed=6091049;
RA Kiodick H.G.; Combratio G.; Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
Nucleic Acids Res. 12:6995-7006(1984)."
CC -----
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CC -----
CC EMBL: X00965; CAA25477.1; ALT_TERM.
DR PIR: A01883; KIHUMK.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV_1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-1 REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AC2P9 CRC64;

Query Match 40.3%; Score 58; DB 1; Length 129;
Best Local Similarity 72.2%; Pred. No. 0.44;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 12 SSGGTDAFPASSLOAED 29
DB 87 SSGGTDFLTITISLQPD 104

RESULT 10
TAT_HV112 STANDARD; PRT; 86 AA.
AC P04326;
DT 20-MAR-1987 (Rel. 04, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (clone 12) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11679;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=66177573; PubMed=3008154;
RA Arya S.K.; Gallo R.C.;
RT "Three novel genes of human T-lymphotropic virus type III: immune
reactivity of their products with sera from acquired immune

RT deficiency syndrome patients.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2209-2213(1986).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC -----
CC EMBL: M1840; AAA44999.1; -.
DR PIR: A04017; TNLJ12.
DR HIV: M1840; TATSPCV12.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat_1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS
SQ SEQUENCE 86 AA; 9758 MW; 4DD609414BEE9115 CRC64;

Query Match 39.6%; Score 57; DB 1; Length 86;
Best Local Similarity 50.0%; Pred. No. 0.39;
Matches 13; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

OY 1 YERKKRRRRSSGTDATAPASSIQ 26
DB 47 YGRKKRRRRRAPSQTHQVLSKQ 72

RESULT 11
TAT_HV1MA STANDARD; PRT; 87 AA.
AC P04613;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TAT protein (Transactivating regulatory protein).
GN TAT.
OS Human immunodeficiency virus type 1 (MA1 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11679;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=66245056; PubMed=2424612;
RA Allizon M.; Wain-Hobson S.; Montagnier L.; Sonigo P.;
RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
of two isolates from African patients.";
RL Cell 46:63-74(1986).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -1- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOLAR.
CC -----
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CC -----
CC EMBL: X04415; CAA28015.1; -.
DR HIV: K03456; TATSMAL.

DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS; PR00055; HIVTATDOMAIN.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
SQ SEQUENCE 87 AA; 10036 MW; 38324128495B1CE CRC64;

Query Match 39.6%; Score 57; DB 1; Length 87;
Best Local Similarity 66.7%; Pred. No. 0.39;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 1 YEKRRRRRRSSGSDA 18
1 | | | | | | | | | |
DB 47 YGRKKRRQRRRRPPGNOA 64

RESULT 12
KV10_HUMAN STANDARD; PRT; 108 AA.
ID KV10_HUMAN
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT specificities";
RL Scand. J. Immunol. 5:677-684(1976).
CC -1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01871; KIHULY.
DR HSSP: P01607; 1RET.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig_V.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOKAIN 1 23 FRAMEWORK-1.
FT DOKAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOKAIN 35 49 FRAMEWORK-2.
FT DOKAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOKAIN 57 88 FRAMEWORK-3.
FT DOKAIN 89 97 FRAMEWORK-4.
FT DOKAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 -108
SQ SEQUENCE 108 AA; 11834 MW; 7399393A95431434A CRC64;

Query Match 39.6%; Score 57; DB 1; Length 108;
Best Local Similarity 72.2%; Pred. No. 0.45;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 12 SGSGTDATAPASSLAQD 29
1 | | | | | | | | | |
DB 65 SGSGTDFPTTSSLOPED 82

RESULT 13
KV10_HUMAN STANDARD; PRT; 108 AA.

AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rel); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Latman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein Rel refined at 2.0-A resolution";
RL Biochemistry 14:4943-4952(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01873; KIHURE.
DR PDB: 1RET; 17-FEB-84.
DR InterPro: IPR003006; Ig_MHC.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOKAIN 1 23 FRAMEWORK-1.
FT DOKAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOKAIN 35 49 FRAMEWORK-2.
FT DOKAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOKAIN 57 88 FRAMEWORK-3.
FT DOKAIN 89 97 FRAMEWORK-4.
FT DOKAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 FRAMEWORK-4.
FT STRAND 4 7
FT STRAND 10 13
FT STRAND 15 16
FT TURN 19 25
FT STRAND 30 31
FT TURN 33 38
FT STRAND 40 41
FT TURN 45 49
FT STRAND 50 52
FT TURN 53 54
FT STRAND 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT TURN 80 82
FT HELIX 85 90
FT STRAND 98 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E118BBCE2A CRC64;

Query Match 39.6%; Score 57; DB 1; Length 108;
Best Local Similarity 72.2%; Pred. No. 0.49;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 12 SGSGTDATAPASSLAQD 29

DB 65 SGGSTDTFTFISSLOPED 82

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RESULT 14
KVLC_HUMAN STANDARD: PRT; 108 AA.
AC P80362;
DN 01-NOV-1995 (Rel. 32, Created)
DN 01-NOV-1995 (Rel. 32, Last sequence update)
DN 15-JUL-1999 (Rel. 38, Last annotation update)
DE 19 kappa chain V-1 region MAT.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE. AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=950806080; PubMed=7993911;
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA Solomon A., Stevens F.J., Schiffer M.;
RT *Comparison of crystal structures of two homologous proteins:
RT structural origin of altered domain interactions in immunoglobulin
RT light-chain dimers.*;
RL Biochemistry 33:14848-14857(1994).
RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA Popp R.A., Solomon A.;
RT *Characterization and preliminary crystallographic data on the VL-
RT related fragment of the human KI Bence Jones protein Mat.*;
RL J. Mol. Biol. 147:185-193(1981).
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; IgV_1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT CONFLICT 30 31 TN -> SD (IN REF. 2).
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11737 MW; DD941B3F0FAE697 CRC64;

```

Query Match 39.6%; Score 57; DB 1; Length 108;
 Best Local Similarity 72.2%; Pred. No. 0.49;
 Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

OY 12 SGGSTDTFTFISSLOPED 29
DB 65 SGGSTDTFTFISSLOPED 82

RESULT 15
KVLC_HUMAN STANDARD: PRT; 108 AA.
AC P01595;
DN 21-JUL-1986 (Rel. 01, Created)
DN 21-JUL-1986 (Rel. 01, Last sequence update)
DN 15-JUL-1999 (Rel. 38, Last annotation update)
DE 19 kappa chain V-1 region BI.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

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OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=73029807; PubMed=4563064;
RA Braun M., Leibold W., Barnikol H.U., Hilschmann N.;
RT *Principle of antibody structure. The primary structure of a
RT monoclonal kappa I-type immunoglobulin L-chain (Bence Jones protein
RT B). 3. The complete amino acid sequence and the genetic
RT significance of the variability principles for the mechanism of
RT antibody formation.*;
RL Hoppe-Sejler's Z. Physiol. Chem. 353:1284-1306(1972).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARRER.
CC PIR: A01863; K1H0B1.
DR HSSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; IgV_1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 12026 MW; 7A83983986A431E7 CRC64;

```

Query Match 38.9%; Score 56; DB 1; Length 108;
 Best Local Similarity 65.0%; Pred. No. 0.67;
 Matches 13; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 10 RRSSTDTFTFISSLOPED 29
 DB 63 RRSSTDTFTFISSLOPED 82

Search completed: July 15, 2002, 13:23:34
 Job time: 1450 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 15, 2002, 13:22:48 ; Search time 172.49 seconds
(without alignments)
29.085 Million cell updates/sec

Title: US-09-712-819A-10

Sequence: 144
1 YERKRRQRRRSGSGTDPATAPASSLQAE D 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp._archaea:*
2: sp._bacteria:*
3: sp._fungi:*
4: sp._human:*
5: sp._invertebrate:*
6: sp._mammal:*
7: sp._mhc:*
8: sp._organelle:*
9: sp._phage:*
10: sp._plant:*
11: sp._rodent:*
12: sp._virus:*
13: sp._vertebrate:*
14: sp._unclassified:*
15: sp._villus:*
16: sp._bacteriap:*
17: sp._archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	45.1	399	10	Q9FTY9 oryza sativ
2	63	43.8	101	15	071973 human immun
3	62	43.1	71	15	040231 human immun
4	62	43.1	444	4	043284 homo sapien
5	62	43.1	1312	4	09NR59 homo sapien
6	62	43.1	1343	4	09H7N4 homo sapien
7	61	42.4	101	15	071968 human immun
8	60.5	42.0	101	15	0902L7 human immun
9	60	41.7	72	15	069622 human immun
10	60	41.7	72	15	P90117 human immun
11	60	41.7	72	15	P90128 human immun
12	60	41.7	101	15	090MK8 human immun
13	60	41.7	829	5	09NEA9 human immun
14	60	41.7	989	5	09NEA9 leishmania
15	59	41.0	72	15	09VDV0 drosophila
16	59	41.0	86	15	P90148 human immun
					09qrb4 human immun

17	59	41.0	101	15	Q902M7	Q902M7 human immun
18	59	41.0	107	4	Q9UL81	Q9UL81 homo sapien
19	58.5	40.6	171	5	Q9N870	Q9N870 leishmania
20	58	40.3	71	15	Q71898	Q71898 human immun
21	58	40.3	71	15	Q71905	Q71905 human immun
22	58	40.3	71	15	Q71919	Q71919 human immun
23	58	40.3	71	15	Q71926	Q71926 human immun
24	58	40.3	71	15	Q71932	Q71932 human immun
25	58	40.3	72	15	P90118	P90118 human immun
26	58	40.3	72	15	P90134	P90134 human immun
27	58	40.3	72	15	P90149	P90149 human immun
28	58	40.3	101	15	Q902P1	Q902P1 human immun
29	58	40.3	107	4	Q96SA9	Q96SA9 homo sapien
30	58	40.3	108	4	Q9UL77	Q9UL77 homo sapien
31	58	40.3	108	4	Q9UL70	Q9UL70 homo sapien
32	57	39.6	72	15	Q70495	Q70495 human immun
33	57	39.6	72	15	Q70501	Q70501 human immun
34	57	39.6	72	15	Q70502	Q70502 human immun
35	57	39.6	72	15	Q70504	Q70504 human immun
36	57	39.6	72	15	Q70507	Q70507 human immun
37	57	39.6	72	15	Q70509	Q70509 human immun
38	57	39.6	72	15	Q70510	Q70510 human immun
39	57	39.6	72	15	Q70512	Q70512 human immun
40	57	39.6	72	15	Q70513	Q70513 human immun
41	57	39.6	72	15	Q70515	Q70515 human immun
42	57	39.6	72	15	Q70526	Q70526 human immun
43	57	39.6	72	15	Q70533	Q70533 human immun
44	57	39.6	72	15	Q70539	Q70539 human immun
45	57	39.6	72	15	P90158	P90158 human immun

ALIGNMENTS

RESULT 1
Q9FTY9 PRELIMINARY: PRT; 399 AA.
ID Q9FTY9
AC Q9FTY9;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE RECEPTOR SER/THR PROTEIN KINASE.
CN P0436F04.9.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone: P0436F04.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF002818; BAB16326.1; -
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR002290; Ser_thr_Pkinase.
DR InterPro: IPR001245; Tyr_Pkinase.
DR Pfam: PF00089; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Kinase; Receptor; Transferase.
SQ SEQUENCE 399 AA; 45329 MW; E2D29FE1F6DAAC7B CRC64;

Query Match 45.1%; Score 65; DB 10; Length 399;
Best Local Similarity 65.0%; Pred. No. 0.31;
Matches 13; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 1 YERRRRRRRRSGGTDA 20
ID 071973 PRELIMINARY; PRT: 101 AA.
AC 071973;
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RC STRAIN-HIV-1NC; PubMed=9765443;
RX MEDLINE=98440562; PubMed=9765443;
RA Wenguo D.M., Novembre F.J.;
RT "Molecular cloning and characterization of viruses isolated from
RT chimpanzees with pathogenic human immunodeficiency virus type 1
RT infections";
RL J. Virol. 72:8976-8987(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-HIV-1NC;
RA Wenguo D.M., Novembre F.J.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
CC EMBL: AF049495; AAC68854.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
SQ SEQUENCE 101 AA; 11439 MW; C13CC065D9DA88B8 CRC64;

Query Match 43.8%; Score 63; DB 15; Length 101;
Best Local Similarity 44.1%; Pred. No. 0.14;
Matches 15; Conservative 4; Mismatches 9; Indels 6; Gaps 1;

OY 1 YERRRRRRRRSGGTDA-----TAPASSIQAE 28
ID 040231 PRELIMINARY; PRT: 71 AA.
AC 040231;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DE TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HE93-A3TAT; PubMed=97335179;
RX MEDLINE=97335179; PubMed=97335179;
RA Kirchhoff P., Greenough T.C., Hamacher M., Sullivan J.L.,
RA Desrosiers R.C.;
RT "Activity of human immunodeficiency virus type 1 promoter/TAR regions
RT and tat genes derived from individuals with different rates of
RT disease progression";

RL Virology 232:319-331(1997).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
CC EMBL: AF000529; AAB62528.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat; 1.
DR PRINTS: PR00055; HIVATDOMAIN.
KW Activator; Nuclear protein; RNA-binding; Transcription regulation.
FT NON_TER 71
SQ SEQUENCE 71 AA; 8162 MW; 5AFB3242E82321B3 CRC64;

Query Match 43.1%; Score 62; DB 15; Length 71;
Best Local Similarity 78.9%; Pred. No. 0.14;
Matches 15; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

OY 1 YERRRRRRRRSGGTDA 17
ID 043284 PRELIMINARY; PRT: 444 AA.
AC 043284;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE LAK-4P.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPHOID;
RA Abe Y., Takakura Y.;
RT "LAK-4 clone from the membrane lymphotoxin expressing subtraction
RT library";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB002405; BAA24179.2; -.
DR InterPro: IPR000515; BPD_transp.
DR PROSITE: PS00402; BPD_TRANS_P_NN_MEMBER; UNKNOWN.1.
SQ SEQUENCE 444 AA; 50427 MW; DD4053A574A00FA1 CRC64;

Query Match 43.1%; Score 62; DB 4; Length 444;
Best Local Similarity 46.4%; Pred. No. 0.91;
Matches 13; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

OY 1 YERRRRRRRRSGGTDAAPASSIQAE 28
ID 414 YERRRRRRSVGTTEAAPPALTDE 441
DB 414 YERRRRRRSVGTTEAAPPALTDE 441

RESULT 5
ID 09NR59 PRELIMINARY; PRT: 1312 AA.
AC 09NR59;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE SER/ARG-RICH PRE-mRNA SPLICING FACTOR SR-A1.
GN SR-A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Scorilas A., Kyriakopoulou L., Katsaros D., Diamandis E.P.;

OX NCBI_TaxID=11676;
RN
RP SEQUENCE FROM N.A.
RC STRAIN-RL22;
RX MEDLINE=95264414; PubMed=7745674;
RA Diaz R.S., Sabino E.C., Mayer A., Mosley J.W., Busch M.P.;
RT "Dual human immunodeficiency virus type 1 infection and recombination
in a dually exposed transfusion recipient. The transfusion safety
study group.";
RL J. Virol. 69:3273-3281(1995).
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANSCRIPTIONAL RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: U11185; AAB78871.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat.1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KM Activator; Nuclear protein; RNA-binding; Transcription regulation.
FT NON_TER 72
SQ SEQUENCE 72 AA; 8331 MW; 4CDD2C4425E67286 CRC64;

Query Match 41.7%; Score 60; DB 15; Length 72;
Best Local Similarity 53.8%; Pred. No. 0.27; Mismatches 10; Gaps 0;
Matches 14; Conservative 2; Indels 0;

OY 1 YERKKRRRRSSGTDATAPASSIQ 26
DB 47 YGRRKKRRRRAPQGNQAHQVLSKQ 72

RESULT 10
P90117
ID P90117 PRELIMINARY; PRT; 72 AA.
AC P90117;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSCRIPTIONAL REGULATOR PROTEIN) (FRAGMENT).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT VE3;
RA Quiñones-Mateu M.E., Domingo E.;
RT "Point mutant frequency and intrasubtype B recombination lead
Venezuelan HIV-1 genetic diversities";
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANSCRIPTIONAL RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: U80463; AAB39113.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat.1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KM Activator; Nuclear protein; RNA-binding; Transcription regulation.
FT NON_TER 72
SQ SEQUENCE 72 AA; 8214 MW; F79D7BBDD0205EEB0 CRC64;

Query Match 41.7%; Score 60; DB 15; Length 72;
Best Local Similarity 64.7%; Pred. No. 0.27;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 YERKKRRRRSSGTD 17
DB 47 YGRRKKRRRRASGSE 63

RESULT 11
P90128
ID P90128 PRELIMINARY; PRT; 72 AA.
AC P90128;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TAT PROTEIN (TRANSCRIPTIONAL REGULATOR PROTEIN) (FRAGMENT).
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT VE18;
RA Quiñones-Mateu M.E., Domingo E.;
RT "Point mutant frequency and intrasubtype B recombination lead
Venezuelan HIV-1 genetic diversities";
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANSCRIPTIONAL RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER (BY SIMILARITY).
DR EMBL: U80477; AAB39127.1; -.
DR InterPro: IPR001831; HIV_Tat.
DR Pfam: PF00539; Tat.1.
DR PRINTS: PR00055; HIVTATDOMAIN.
KM Activator; Nuclear protein; RNA-binding; Transcription regulation.
FT NON_TER 72
SQ SEQUENCE 72 AA; 8337 MW; 4D0AED1145E6645C CRC64;

Query Match 41.7%; Score 60; DB 15; Length 72;
Best Local Similarity 53.8%; Pred. No. 0.27; Mismatches 10; Gaps 0;
Matches 14; Conservative 2; Indels 0;

OY 1 YERKKRRRRSSGTDATAPASSIQ 26
DB 47 YGRRKKRRRRSPGSGTHQVLSKQ 72

RESULT 12
O90MK8
ID O90MK8 PRELIMINARY; PRT; 101 AA.
AC O90MK8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TAT PROTEIN.
GN TAT.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN
RP SEQUENCE FROM N.A.
RC STRAIN-ARMA159;
RA Carr J.K., Avila M., Gomez-Carrillo M., Salomon H., Hierholzer J.,
RA Matanavearedj V., Pando M., Negrete M., Russell K., Sanchez J.,
RA Bix D., Andrade R., Vinholes J., McCutchan F.;
RT "Diverse BF recombinants have spread widely since the introduction of
HIV-1 into South America.";
RL AIDS 0:0-0(2001).
RN
RP SEQUENCE FROM N.A.
RC STRAIN-ARMA159;
RA Carr J.K., Avila M., Gomez-Carrillo M., Salomon H., Hierholzer J.,
RA Matanavearedj V., Pando M., Negrete M., Russell K., Sanchez J.,
RA Bix D., Andrade R., Vinholes J., McCutchan F.;
RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF385936; AAK69333.1; -.
SQ SEQUENCE 101 AA; 11416 MW; 360605029A87A327 CRC64;

KA MEDLINE=9904962/; PubMed=9833881;

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OW protein - protein search, using sw model

Run on: July 15, 2002, 12:57:59 ; Search time 228.39 Seconds

(without alignments)
14.104 Million cell updates/sec

Title: US-09-712-819a-10

Perfect score: 144

Sequence: 1 YERRKRRORRRSGCTDATAPASLAQAD 29

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: A_Geneseq_032802.*
2: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1980.DAT.*
3: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1981.DAT.*
4: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1982.DAT.*
5: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1983.DAT.*
6: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1984.DAT.*
7: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1985.DAT.*
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22: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA2000.DAT.*
23: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	43.8	82	19	AAW62807
2	63	43.8	94	19	AAW62808
3	63	43.8	107	20	AAV05269
4	63	43.8	111	15	AAW52059
5	63	43.8	112	18	AAW27527
6	63	43.8	113	15	AAW50313
7	63	43.8	113	15	AAW50314
8	63	43.8	113	17	AAW98489
9	63	43.8	113	19	AAW42466
10	63	43.8	113	21	AAW18857
11	63	43.8	113	21	AAW18861

12	63	43.8	113	21	AAW18863	Amino acid sequenc
13	63	43.8	113	21	AAW18869	Amino acid sequenc
14	63	43.8	113	21	AAW18871	Amino acid sequenc
15	63	43.8	113	21	AAW18873	Amino acid sequenc
16	63	43.8	113	21	AAW18879	Amino acid sequenc
17	63	43.8	113	21	AAW18881	Amino acid sequenc
18	63	43.8	113	22	AAW62769	Human HIV-1 monoclonal antibody
19	63	43.8	114	14	AAW30144	Anti-GM-CSF monoclonal antibody
20	63	43.8	114	15	AAW45605	Anti-IL-12 monoclonal antibody
21	63	43.8	114	18	AAW15537	Anti-IL-12 monoclonal antibody
22	63	43.8	115	15	AAW27546	Human Ab light chain
23	63	43.8	120	18	AAW61240	Monoclonal antibody
24	63	43.8	120	22	AAW65565	Amino acid sequenc
25	63	43.8	124	20	AAW57181	Amino acid sequenc
26	63	43.8	126	22	AAW77598	Anti-human VEGF receptor
27	63	43.8	126	22	AAW78667	Anti-human IL-12 monoclonal antibody
28	63	43.8	127	17	AAW06443	Anti-human IL-12 monoclonal antibody
29	63	43.8	131	16	AAW75355	Humanized antibody
30	63	43.8	131	16	AAW70202	Humanized antibody
31	63	43.8	131	20	AAW23779	Light chain variab
32	63	43.8	131	20	AAW23771	Light chain variab
33	63	43.8	131	20	AAW18126	Light chain sequen
34	63	43.8	131	20	AAW18118	Light chain sequen
35	63	43.8	132	21	AAW07966	A light chain vari
36	63	43.8	133	9	AAW80894	V region of L chain
37	63	43.8	133	18	AAW21934	Variable light sub
38	63	43.8	133	20	AAW05264	Antibody 24-31 hum
39	63	43.8	134	21	AAW50690	Human Hum4 VL Clai
40	63	43.8	135	21	AAW03714	Immunoglobulin kap
41	63	43.8	137	18	AAW10547	Wild type murine a
42	63	43.8	137	18	AAW10544	Humanised murine a
43	63	43.8	137	18	AAW10545	Humanised murine a
44	63	43.8	147	20	AAW34314	IgM antibody CEM 1
45	63	43.8	149	20	AAW34311	IgM antibody CEM 1

ALIGNMENTS

RESULT 1	
AAW62807	
ID	AAW62807 standard; Peptide: 82 AA.
AC	AAW62807;
DT	23-SEP-1998 (first entry)
XX	Amino acid sequence of a human antibody fragment.
DE	
XX	Human: immunoglobulin: Ig; transgenic; non-human mammal;
KW	inactivated endogenous Ig locus; B-cell development;
KW	human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
KW	kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
KW	production; antibody.
XX	
OS	Homo sapiens.
XX	
PN	W09824893-AZ.
XX	
PD	11-JUN-1998.
XX	
PF	03-DEC-1997; 97W0-US23091.
XX	
PR	03-DEC-1996; 96US-0759620.
XX	
PA	(ABGE-) ABGENIX INC.
XX	
PI	Green L, Jakobovits A, Klapholz S, Kucherlapati R;
XX	Mendez M.
DR	WPI; 1998-333314/29.
XX	
PT	New transgenic non-human mammals - having an inactivated

PT Immunoglobulin locus and a near complete human immunoglobulin locus,
PT used for production of human antibodies
XX
PS Disclosure: Page 78; 128pp; English.
XX
CC AAW6793-822 represent fragments of human antibodies produced by
CC transgenic Xenomice, created using the method of the invention. The
CC specification describes a transgenic non-human mammal which has genome
CC modifications that comprise an inactivated endogenous immunoglobulin (Ig)
CC locus, so that the mammal does not display normal B-cell development. The
CC modified genome also has an inserted human heavy chain Ig locus in
CC germine configuration, the human heavy chain Ig locus comprising a human
CC micro constant region and regulatory and switch sequences, human J-H
CC genes, human D-H genes, and human V-H genes and an inserted human kappa
CC light chain Ig locus in germine configuration, the human kappa light
CC chain Ig locus comprising a human kappa constant region, J-kappa genes,
CC and V-kappa genes, where the number of V-H and V-kappa genes inserted
CC are selected to restore normal B-cell development in the mammal. The
CC transgenic animals have a near complete human Ig locus, including both a
CC human heavy chain locus and a human kappa light chain locus. They can
CC be used for the production of human antibodies when exposed to
CC particular antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha
CC the mice will produce antibodies to IL-8, EGFR or TNF- alpha
CC respectively.
XX
XX Sequence 82 AA:
SQ
Query Match 43.8%; Score 63; DB 19; Length 82;
Best Local Similarity 77.8%; Pred. No. 0.2;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 12 SCGCTDATTAPASSLQAE 29
Db ||||| |||||
52 sgsqdflltllsslqae 69
RESULT 2
AAW62808
ID AAW62808 standard; Peptide: 94 AA.
XX
AC AAW62808;
XX
DT 23-SEP-1998 (first entry)
XX
DE Amino acid sequence of a human antibody fragment.
XX
KW Human; Immunoglobulin; Ig; transgenic; non-human mammal;
KW inactivated endogenous Ig locus; B-cell development;
KW human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
KW kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
KW production; antibody.
XX
XX Homo sapiens.
OS
XX
PN WO9824893-A2.
XX
PD 11-JUN-1998.
XX
PE 03-DEC-1997; 97WO-US23091.
XX
PR 03-DEC-1996; 96US-0759620.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Green L, Jakobovits A, Klapholz S, Kuchertlappal R;
PI Mendez M;
XX
XX WPI: 1998-333314/29.
XX
PT New transgenic non-human mammals - having an inactivated
PT immunoglobulin locus and a near complete human immunoglobulin locus,
PT used for production of human antibodies

XX
PS Disclosure: Page 79; 128pp; English.
XX
XX AAW6793-822 represent fragments of human antibodies produced by
CC transgenic Xenomice, created using the method of the invention. The
CC specification describes a transgenic non-human mammal which has genome
CC modifications that comprise an inactivated endogenous immunoglobulin (Ig)
CC locus, so that the mammal does not display normal B-cell development. The
CC modified genome also has an inserted human heavy chain Ig locus in
CC germine configuration, the human heavy chain Ig locus comprising a human
CC micro constant region and regulatory and switch sequences, human J-H
CC genes, human D-H genes, and human V-H genes and an inserted human kappa
CC light chain Ig locus in germine configuration, the human kappa light
CC chain Ig locus comprising a human kappa constant region, J-kappa genes,
CC and V-kappa genes, where the number of V-H and V-kappa genes inserted
CC are selected to restore normal B-cell development in the mammal. The
CC transgenic animals have a near complete human Ig locus, including both a
CC human heavy chain locus and a human kappa light chain locus. They can
CC be used for the production of human antibodies when exposed to
CC particular antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha
CC the mice will produce antibodies to IL-8, EGFR or TNF- alpha
CC respectively.
XX
XX Sequence 94 AA:
SQ
Query Match 43.8%; Score 63; DB 19; Length 94;
Best Local Similarity 77.8%; Pred. No. 0.24; 4; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 12 SCGCTDATTAPASSLQAE 29
Db ||||| |||||
52 sgsqdflltllsslqae 69
RESULT 3
AAV05269
ID AAV05269 standard; Protein: 107 AA.
XX
AC AAV05269;
XX
DT 21-JUN-1999 (first entry)
XX
DE Antibody 24-31 humanised VL chain sequence.
XX
KW Antibody 24-31; variable light chain; humanised antibody; gene therapy;
KW CD40 binding inhibitor; gp39; autoimmune disease; food-related allergy;
KW graft-versus-host disease; graft rejection; intestinal inflammation;
KW reversible obstructive airways disease; allergy; transplant rejection;
KW asthma; leukaemia; lymphoma; immunosuppressant; cellular therapy;
KW immune response inhibitor; cancer.
XX
XX Mus sp.
OS
XX Homo sapiens.
OS
XX Synthetic.
XX
PN WO9912566-A1.
XX
PD 18-MAR-1999.
XX
PE 08-SEP-1998; 98WO-US18163.
XX
PR 08-SEP-1997; 97US-0925339.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Black A, Hanna N, Newman RA, Padlan EA;
PI
XX
XX WPI: 1999-229142/19.
XX
XX New humanized antibodies to human gp30
XX
PS Claim 7; Page 84; 122pp; English.

XX This sequence is the variable light chain of a humanised antibody of
 CC the invention. The antibody is capable of competing with a murine 24-31
 CC antibody for inhibiting CD40 binding to gp39. The humanised antibodies
 CC can be used for the treatment of a disease treatable by modulating gp39
 CC expression or inhibiting the gp39/CD40 interaction. They can be used for
 CC treating e.g. autoimmune diseases such as rheumatoid arthritis, psoriasis
 CC multiple sclerosis, diabetes, systemic lupus erythematosus and idiopathic
 CC thrombocytopenic purpura (ITP) or non-autoimmune conditions such as
 CC graft-versus-host disease (GVHD) or graft rejection. They can also be
 CC used for the treatment of reversible obstructive airways disease,
 CC intestinal inflammations and allergies (e.g. coeliac disease, Crohn's
 CC disease and ulcerative colitis) and food-related allergies (e.g.
 CC migraine, rhinitis and eczema), transplant rejection, asthma, leukaemia,
 CC or lymphoma. The antibodies can also be used as immunosuppressants, in
 CC particular during gene or cellular therapy. They may be used to inhibit
 CC humoral and cellular immune responses against viral vectors, e.g.
 CC retroviral vectors or adenoviral vectors. The use of such antibodies
 CC should enable such cells or vectors to be administered repeatedly, which
 CC will facilitate treatment of chronic diseases such as cancers and
 CC autoimmune diseases.

XX Sequence 107 AA:

Query Match 43.8%; Score 63; DB 20; Length 107;
 Best Local Similarity 77.8%; Pred. No. 0.27;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGSGTDATAPASSLQAED 29
 ||||| | |||||
 Db 65 ssgsgtdfltlslsigaed 82

RESULT 4

ID AAR52059 standard; Protein; 111 AA.

XX AAR52059;

DT 10-OCT-1996 (first entry)

XX Light chain variable region of human KV4B antibody.

XX antibody; humanised; murine; human; heavy chain; light; variable;
 KW framework region; complementarity determining region; reshaping;
 KW modelling; surface residue; modify.

XX Homo sapiens.

XX Location/Qualifiers

FT Key 1..23 /label=framework_region_1

FT Region /note="FR 1"

FT Region 24..40 /label=framework_region_1

FT Region /note="CDR 1"

FT Region 41..55 /note="FR 2"

FT Region 56..62 /note="CDR 2"

FT Region 63..95 /note="FR 3"

FT Region 96..104 /note="CDR 3"

FT Region /note="CDR 3"

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

FT Region

XX (PEDE/) PEDERSEN J T.
 PA (IMMU-) IMMUNOGEN INC.
 XX Guild BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;
 DR WPI: 1994-120230/15.

XX Method of resurfacing of rodent antibodies to produce humanised
 PT antibody forms - for producing non-human antibodies with improved
 PT therapeutic efficiency by presenting human surface on V-region
 XX Example 1; Fig 4A: 230pp; English.

XX Modification of a rodent antibody (Ab) or fragment by resurfacing in
 CC order to produce a humanised rodent Ab can be determined by calculating
 CC homology between murine and human Ab antibody surfaces. In order to test
 CC the resurfacing approach of the invention, three humanisation
 CC experiments were set up: (1) traditional loop grafting; (2) resurfacing
 CC approach using most similar chain; and (3) resurfacing approach using
 CC human sequences with most similar surface residues. The Ab used was the
 CC murine anti-N901 Ab (see AAR52055). Experiment 3 was carried out using
 CC the present sequence which represents the human KV4B Ab light chain
 CC variable region with 71 percent homology with anti-N901 Ab. N901/KV4B
 CC (AAR52060) was prepd. by resurfacing.

XX Sequence 111 AA:

Query Match 43.8%; Score 63; DB 15; Length 111;
 Best Local Similarity 77.8%; Pred. No. 0.28;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGSGTDATAPASSLQAED 29
 ||||| | |||||
 Db 70 ssgsgtdfltlslsigaed 87

RESULT 5

ID AAW27527 standard; Protein; 112 AA.

XX AAW27527;

DT 16-DEC-1997 (first entry)

XX Light chain variable region of human CRA2 antibody.

XX Complementarity determining region; CDR; murine; mouse; human;
 KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
 KW IGF; MAb; light chain; variable region; humanised; semi-chimeric;
 KW chimeric; treatment; prevention; disease; allergy; CRA2.

XX Homo sapiens.

XX JF09J91686-A.

XX 29-JUL-1997.

XX 19-JAN-1996; 96JP-0024816.

XX 19-JAN-1996; 96JP-0024816.

XX (ASAK) ASAKI BREWERIES LTD.

XX (NIKK-) NIKKA WHISKEY KK.

XX (TORI) TORI YAKUHIN KK.

XX (TSUR/) TSURA T.

XX WPI: 1997-429186/40.

XX Humanised, semi-chimeric and chimeric antibodies against human

XX high-affinity IGE receptor - useful medicinally and have low

XX antigenicity in humans

XX Claim 2; Page 14; 26pp; Japanese.
XX
XX The present sequence, the light chain variable region of the human
CC antibody (Ab) CHA2, was used in the preparation of a humanised or
CC semi-chimeric monoclonal Ab (Mab), comprising complementarity
CC determining regions (CDR) from a murine, anti-human high affinity
CC immunoglobulin E (IgE) receptor, Mab. The humanised, semi-chimeric
CC or chimeric Mab can be used to treat or prevent diseases,
CC specifically allergies, associated with the receptor, and has very
CC low antigenicity in humans.
XX
SQ Sequence 112 AA:

Query Match 43.8%; Score 63; DB 18; Length 112;
Best Local Similarity 77.8%; Pred. No. 0.28;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 12 SSGCTDATAPASSLOAED 29
Db 69 ssgctdftlttslsged 86

RESULT 6
AAR50313
ID AAR50313 standard; Protein; 113 AA.
XX
AC AAR50313;
XX
DT 05-OCT-1994 (first entry)
XX
DE Humanised light chain variable region pfhzlcl-1.
XX
KW Monoclonal antibody; Plasmodium falciparum; CDR;
KW complementarity determining region; fusion protein;
KW murine; variable; light; heavy; chain; malaria.
XX
CS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 24..40
FT /Label= CDR1
FT Region 56..62
FT /Label= CDR2
FT Region 95..103
FT /Label= CDR3
XX
XX WO9405690-A.
XX
XX 17-MAR-1994.
XX
XX 08-SEP-1993; 93WO-US08435.
XX
XX 09-SEP-1992; 92US-0941654.
XX
XX (SMK) SMITHKLINE BEECHAM CORP.
XX (USNA) US SEC OF ARMY.
XX (USNA) US SEC OF NAVY.
XX
XX Charoenyit Y, Hoffman S, Hurle M, Rosenberg M;
XX Sadoff JC, Sylvester DR, Gross MS;
XX WPI: 1994-101115/12.
XX N-PDB; AAQ44827.
XX
XX New engineered antibodies and fusion proteins for preventing
PT Plasmodium infection - contg. murine antibody CDR sequences, and
PT corresp. nucleic acid, vectors and transformed cells
XX
XX Claim 5; Fig 2; 98pp; English.
XX
XX Naturally-occurring (AAQ44841-42) and synthetic (AAQ44825-28)

CC variable light chain and variable heavy chain sequences
CC derived from murine mAb NFS2 are provided. Murine mAb NFS2,
CC its variable chain peptides, CDRs, functional fragments,
CC Fab fragments, and analogs are useful in prodn. of fusion
CC proteins, esp. engineered antibodies. These prods. are
CC used to protect humans against Plasmodium infections.
XX
SQ Sequence 113 AA:

Query Match 43.8%; Score 63; DB 15; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.29;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 12 SSGCTDATAPASSLOAED 29
Db 71 ssgctdftlttslsged 88

RESULT 7
AAR50314
ID AAR50314 standard; Protein; 113 AA.
XX
AC AAR50314;
XX
DT 05-OCT-1994 (first entry)
XX
DE Humanised light chain variable region pfhzlcl-2.
XX
KW Monoclonal antibody; Plasmodium falciparum; CDR;
KW complementarity determining region; fusion protein;
KW murine; variable; light; heavy; chain; malaria.
XX
CS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 24..40
FT /Label= CDR1
FT Region 56..62
FT /Label= CDR2
FT Region 95..103
FT /Label= CDR3
XX
XX WO9405690-A.
XX
XX 17-MAR-1994.
XX
XX 08-SEP-1993; 93WO-US08435.
XX
XX 09-SEP-1992; 92US-0941654.
XX
XX (SMK) SMITHKLINE BEECHAM CORP.
XX (USNA) US SEC OF ARMY.
XX (USNA) US SEC OF NAVY.
XX
XX Charoenyit Y, Hoffman S, Hurle M, Rosenberg M;
XX Sadoff JC, Sylvester DR, Gross MS;
XX WPI: 1994-101115/12.
XX N-PDB; AAQ44828.
XX
XX New engineered antibodies and fusion proteins for preventing
PT Plasmodium infection - contg. murine antibody CDR sequences, and
PT corresp. nucleic acid, vectors and transformed cells
XX
XX Claim 5; Fig 3; 98pp; English.
XX
XX Naturally-occurring (AAQ44841-42) and synthetic (AAQ44825-28)
CC variable light chain and variable heavy chain sequences
CC derived from murine mAb NFS2 are provided. Murine mAb NFS2,
CC its variable chain peptides, CDRs, functional fragments,
CC Fab fragments, and analogs are useful in prodn. of fusion
CC proteins, esp. engineered antibodies. These prods. are

```
CC used to protect humans against Plasmodium infections.
XX
SO Sequence 113 AA:

Query Match 43.8%; Score 63; DB 15; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.29;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SGGCTDATAPASS1QAED 29
   ||||| | |||||
   71 sgsydtftltlsslqsd 88
Db

RESULT 8
AAR98489
ID AAR98489 standard; Protein; 113 AA.
AC AAR98489;
DT 12-OCT-1996 (first entry)
DE Humanised 2B6 antibody light chain variable region.
XX
XX Antibody engineering; humanised antibody; chimeric antibody; Fab;
KW Interleukin-5; IL-5; eosinophil; asthma; allergic rhinitis;
KM atopic dermatitis; therapy; diagnosis; light chain; VL;
XX monoclonal antibody; MAb.
XX
XX Synthetic.
XX
FH Key 1..23 Location/Qualifiers
FT Region /note= "human LEN framework region"
FT Region 24..40 /label= CDR1
FT /note= "mouse MAb 2B6 VL CDR1"
FT Region 41..55 /note= "human LEN framework region"
FT /note= "mouse MAb 2B6 VL CDR2"
FT Region 56..62 /label= CDR2
FT /note= "mouse MAb 2B6 VL CDR2"
FT Region 63..94 /note= "human LEN framework region"
FT /label= CDR3
FT /note= "mouse MAb 2B6 VL CDR3"
FT Region 104..113 /note= "human LEN framework region"
FT
XX
XX W09621000-A2.
XX
XX 11-JUL-1996.
XX
XX 22-DEC-1995; 95WO-US17082.
XX
XX 06-JUN-1995; 95US-0470110.
XX 23-DEC-1994; 94US-0363131.
XX 06-JUN-1995; 95US-0467420.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Ames RS, Appelbaum ER, Chaiken IM, Cook RM, Gross MS;
XX Holmes SD, McMillan LJ, Theisen TW;
XX
XX WPI: 1996-333976/33.
XX N-PSDB: AAT34094.
XX
XX New monoclonal antibody to human interleukin-5 - used to produce
XX products for the treatment and diagnosis of conditions associated
XX with excess eosinophil produ., e.g asthma etc.
XX
```

```
PS Claim 14; Page 55-56; 120pp; English.
XX
XX The light chain variable region (AAR98489) of humanised antibody 2B6
XX comprises complementarity determining regions (see also AAR98484-86)
XX derived from murine monoclonal antibody 2B6 VL (see also AAR98479) and
XX framework regions from human Bence-Jones protein (LEN). Murine 2B6
XX is specific for human interleukin-5 (IL-5). The humanised VL was
XX expressed in COS cells using vector pCDL5HZUC1.0 (AAT34110) carrying
XX a VL-encoding DNA construct (AAT34094). Humanised 2B6 VL was also
XX produced (see also AAR98488). Humanised 2B6 can be used for the
XX diagnosis and treatment of IL-5-mediated conditions, e.g. asthma,
XX allergic rhinitis and atopic dermatitis.
XX
XX Sequence 113 AA:

Query Match 43.8%; Score 63; DB 17; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.29;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SGGCTDATAPASS1QAED 29
   ||||| | |||||
   71 sgsydtftltlsslqsd 88
Db

RESULT 9
AAW42466
ID AAW42466 standard; Protein; 113 AA.
AC AAW42466;
XX
XX 22-JUN-1998 (first entry)
XX
XX Interleukin-5 humanised light chain variable region.
XX
XX Neutralising antibody; monoclonal antibody; MAb; 2B6; LEN; mouse;
KW Interleukin-5; IL-5; human; eosinophil; asthma; allergic rhinitis;
KM atopic dermatitis; therapy; diagnosis; humanised antibody.
XX
XX Chimeric - Mus musculus.
XX
XX Chimeric - Homo sapiens.
XX
XX Key 1..23 Location/Qualifiers
FH Region /label= FR1
FT /note= "LEN framework region 1"
FT Region 24..40 /label= CDR1
FT /note= "2B6 complementarity determining region 1"
FT Region 41..55 /label= FR2
FT /label= FR2
FT /note= "LEN framework region 2"
FT Region 56..62 /label= CDR2
FT /note= "2B6 complementarity determining region 2"
FT Region 63..94 /label= FR3
FT /label= FR3
FT /note= "LEN framework region 3"
FT Region 95..103 /label= CDR3
FT /note= "2B6 complementarity determining region 3"
FT /label= FR4
FT /note= "LEN framework region 4"
FT
XX
XX W09748418-A1.
XX
XX 24-DEC-1997.
XX
XX 20-JUN-1997; 97WO-US10769.
XX
XX 21-JUN-1996; 96US-0667769.
XX
```

PA (SMK) SMITHKLINE BEECHAM CORP.
XX
PI Appelbaum ER, Cook RM;
XX
XX WPI: 1998-062853/06.
DR N-PSDB; AAV03497.
XX
XX Use of neutralising antibody to human Interleukin-5 - that does not
PT block binding to receptor alpha chain, to treat e.g. asthma.
XX allergic rhinitis or atopic dermatitis
XX
XX Example 4; Fig 9; 116pp; English.
XX
XX This polypeptide comprises a humanised antibody light chain
CC variable region composed of human LEN framework regions and
CC complementarity determining regions (see AAW42460-62) derived from
CC anti-human interleukin-5 (hIL-5) murine monoclonal antibody (MAb)
CC 2B6 light chain (see AAW42452). It is encoded by a DNA construct
CC (see AAW03497) in vector pCMTLSHZC1.0 (see AAW03504). The humanised
CC light chain has been expressed in transfected COS host cells. The
CC humanised antibodies, especially altered, chimeric and
CC neutralising antibodies which are characterised by hIL-5 specificity,
CC are useful for treating hIL-5-mediated disorders such as asthma,
CC allergic rhinitis and atopic dermatitis, and can also be used in
CC the diagnosis of such conditions by measurement (e.g. by ELISA) of
CC host cells for expression of the novel antibodies.
XX
XX Sequence 113 AA:
SQ
Query Match 43.8%; Score 63; DB 19; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.29;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 12 SSGCTDATAPASSLQAD 29
DB 71 ssgctdftltlslgaed 88
RESULT 10
AA18857
ID AA18857 standard; Protein; 113 AA.
XX
XX AAB18857;
XX
XX 08-FEB-2001 (first entry)
XX
XX Amino acid sequence of anti-p53 antibody light chain clone 163.2.
XX
XX p53; antibody; immune response; vaccine; gene therapy; cancer;
XX rheumatoid arthritis; coronary heart disease.
XX
XX Homo sapiens.
XX
XX MO200056770-A1.
XX
XX 28-SEP-2000.
XX
XX 15-MAR-2000; 2000MO-AU00189.
XX
XX 19-MAR-1999; 99AU-0009321.
XX
XX (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
XX
XX Ward RL, Coomber DMJ;
XX
XX WPI: 2000-638249/61.
XX N-PSDB; AAA96134.
XX
XX Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
PT fragments, useful in treatment and diagnosis of cancer, rheumatoid

PT arthritis and coronary heart disease -
XX
XX Claim 30; Page 132; 163pp; English.
XX
XX The present sequence represents the light chain of an antibody reactive
CC against p53. The antibody is obtained from a vertebrate host expressing
CC an immune response against a naturally occurring disease. The antibodies
CC are useful in pharmaceutical compositions, which additionally contain
CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
CC or gadolinium. The polypeptide components of the antibodies are useful in
CC vaccines, for inducing an immune response against a disease in a
CC vertebrate, for treatment and/or prophylaxis of disease and for detection
CC purposes. The nucleic acid sequences can be used to detect a disease as
CC well as for gene therapy and recombinant production of the polypeptides.
CC In particular, the following can be treated cancer, rheumatoid arthritis
CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
CC of epithelial origin, e.g. colo-rectal cancer, breast cancer, lung cancer,
CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.
XX
XX Sequence 113 AA:
SQ
Query Match 43.8%; Score 63; DB 21; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.29;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 12 SSGCTDATAPASSLQAD 29
DB 71 ssgctdftltlslgaed 88
RESULT 11
AAB18861
ID AAB18861 standard; Protein; 113 AA.
XX
XX AAB18861;
XX
XX 08-FEB-2001 (first entry)
XX
XX Amino acid sequence of anti-p53 antibody light chain clone 163.6.
XX
XX p53; antibody; immune response; vaccine; gene therapy; cancer;
XX rheumatoid arthritis; coronary heart disease.
XX
XX Homo sapiens.
XX
XX MO200056770-A1.
XX
XX 28-SEP-2000.
XX
XX 15-MAR-2000; 2000MO-AU00189.
XX
XX 19-MAR-1999; 99AU-0009321.
XX
XX (SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
XX
XX Ward RL, Coomber DMJ;
XX
XX WPI: 2000-638249/61.
XX N-PSDB; AAA96138.
XX
XX Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
PT arthritis and coronary heart disease -
XX
XX Claim 30; Page 136; 163pp; English.
XX
XX The present sequence represents the light chain of an antibody reactive
CC against p53. The antibody is obtained from a vertebrate host expressing
CC an immune response against a naturally occurring disease. The antibodies

are useful in pharmaceutical compositions, which additionally contain chelators, drugs, prodrugs, toxins and imaging markers e.g. radioisotopes or gadolinium. The polypeptide components of the antibodies are useful in vaccines, for inducing an immune response against a disease in a vertebrate, for treatment and/or prophylaxis of disease and for detection purposes. The nucleic acid sequences can be used to detect a disease as well as for gene therapy and recombinant production of the polypeptides. In particular, the following can be treated cancer, rheumatoid arthritis and coronary heart disease. Cancers include carcinogenic tumours, tumours of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer, head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer, gastric cancer, brain cancer, bladder cancer, prostate cancer and urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours, e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

Sequence 113 AA;

Query Match 43.8%; Score 63; DB 21; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.29;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

12 SSGSGDTATAPASSLQAE 29
||||| | |||||
71 ssgsgdtatltslsgaed 88

RESULT 12
AAB18863 standard; Protein; 113 AA.
AAB18863;
08-FEB-2001 (first entry)

Amino acid sequence of anti-p53 antibody light chain clone 163.7.

p53; antibody; immune response; vaccine; gene therapy; cancer;
rheumatoid arthritis; coronary heart disease.

Homo sapiens.

Key Location/Qualifiers
Misc-difference 101 /note="Arg encoded by CCA"

MO200056770-A1.
28-SEP-2000.
15-MAR-2000; 2000MC-AU00189.
19-MAR-1999; 99AU-0009321.
(SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
Ward RL, Coomber DMJ;
WPI; 2000-638249/61.
N-PSDB; AAA96140.

Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide fragments, useful in treatment and diagnosis of cancer, rheumatoid arthritis and coronary heart disease

Claim 30; Page 138; 163pp; English.

The present sequence represents the light chain of an antibody reactive against p53. The antibody is obtained from a vertebrate host expressing an immune response against a naturally occurring disease. The antibodies are useful in pharmaceutical compositions, which additionally contain chelators, drugs, prodrugs, toxins and imaging markers e.g. radioisotopes or gadolinium. The polypeptide components of the antibodies are useful in

vaccines, for inducing an immune response against a disease in a vertebrate, for treatment and/or prophylaxis of disease and for detection purposes. The nucleic acid sequences can be used to detect a disease as well as for gene therapy and recombinant production of the polypeptides. In particular, the following can be treated cancer, rheumatoid arthritis and coronary heart disease. Cancers include carcinogenic tumours, tumours of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer, head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer, gastric cancer, brain cancer, bladder cancer, prostate cancer and urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours, e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

Sequence 113 AA;

Query Match 43.8%; Score 63; DB 21; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.29;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

12 SSGSGDTATAPASSLQAE 29
||||| | |||||
71 ssgsgdtatltslsgaed 88

RESULT 13
AAB18869 standard; Protein; 113 AA.
AAB18869;
08-FEB-2001 (first entry)

Amino acid sequence of anti-p53 antibody light chain clone 163.15.

p53; antibody; immune response; vaccine; gene therapy; cancer;
rheumatoid arthritis; coronary heart disease.

Homo sapiens.

MO200056770-A1.
28-SEP-2000.
15-MAR-2000; 2000MC-AU00189.
19-MAR-1999; 99AU-0009321.
(SVIN-) ST VINCENT'S HOSPITAL SYDNEY LTD.
Ward RL, Coomber DMJ;
WPI; 2000-638249/61.
N-PSDB; AAA96146.

Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide fragments, useful in treatment and diagnosis of cancer, rheumatoid arthritis and coronary heart disease

Claim 30; Page 144; 163pp; English.

The present sequence represents the light chain of an antibody reactive against p53. The antibody is obtained from a vertebrate host expressing an immune response against a naturally occurring disease. The antibodies are useful in pharmaceutical compositions, which additionally contain chelators, drugs, prodrugs, toxins and imaging markers e.g. radioisotopes or gadolinium. The polypeptide components of the antibodies are useful in vaccines, for inducing an immune response against a disease in a vertebrate, for treatment and/or prophylaxis of disease and for detection purposes. The nucleic acid sequences can be used to detect a disease as well as for gene therapy and recombinant production of the polypeptides. In particular, the following can be treated cancer, rheumatoid arthritis and coronary heart disease. Cancers include carcinogenic tumours, tumours of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,

CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
 CC gastric cancer, brain cancer, bladder cancer, prostate cancer and
 CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
 CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

Sequence 113 AA:

Query Match 43.8%; Score 63; DB 21; Length 113;
 Best Local Similarity 77.8%; Pred. No. 0.29;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGGDTATAPASSLQAD 29
 ||||| | |||||
 Db 71 ssggdtfltlsslqad 88

RESULT 14

AA1871 standard; Protein; 113 AA.

AC AA1871:

DT 08-FEB-2001 (first entry)

DE Amino acid sequence of anti-p53 antibody light chain clone 163.16.

KW p53; antibody; immune response; vaccine; gene therapy; cancer;
 KW rheumatoid arthritis; coronary heart disease.

OS Homo sapiens.

PN W0200056770-A1.

PD 28-SEP-2000.

PF 15-MAR-2000; 2000WO-AU00189.

PR 19-MAR-1999; 99AU-0009321.

PA (SVLN-) ST VINCENT'S HOSPITAL SYDNEY LTD.

PI Ward RL, Coomber DMJ;

DR WPI: 2000-638249/61.
 N-PSDB; AAA96148.

PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
 PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
 PT arthritis and coronary heart disease -

PS Claim 30: Page 146; 163pp; English.

CC The present sequence represents the light chain of an antibody reactive
 CC against p53. The antibody is obtained from a vertebrate host expressing
 CC an immune response against a naturally occurring disease. The antibodies
 CC are useful in pharmaceutical compositions, which additionally contain
 CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
 CC or gadolinium. The polypeptide components of the antibodies are useful in
 CC vaccines, for inducing an immune response against a disease in a
 CC vertebrate, for treatment and/or prophylaxis of disease and for detection
 CC purposes. The nucleic acid sequences can be used to detect a disease as
 CC well as for gene therapy and recombinant production of the polypeptides.
 CC In particular, the following can be treated cancer, rheumatoid arthritis
 CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
 CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
 CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
 CC gastric cancer, brain cancer, bladder cancer, prostate cancer, and
 CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
 CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

Sequence 113 AA:

Query Match 43.8%; Score 63; DB 21; Length 113;
 Best Local Similarity 77.8%; Pred. No. 0.29;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGGDTATAPASSLQAD 29
 ||||| | |||||
 Db 71 ssggdtfltlsslqad 88

RESULT 15

AA1873 standard; Protein; 113 AA.

AC AA1873:

DT 08-FEB-2001 (first entry)

DE Amino acid sequence of anti-p53 antibody light chain clone 163.17.

KW p53; antibody; immune response; vaccine; gene therapy; cancer;
 KW rheumatoid arthritis; coronary heart disease.

OS Homo sapiens.

PN W0200056770-A1.

PD 28-SEP-2000.

PF 15-MAR-2000; 2000WO-AU00189.

PR 19-MAR-1999; 99AU-0009321.

PA (SVLN-) ST VINCENT'S HOSPITAL SYDNEY LTD.

PI Ward RL, Coomber DMJ;

DR WPI: 2000-638249/61.
 N-PSDB; AAA96150.

PT Polynucleotides encoding anti-p53 antibodies, polypeptides and peptide
 PT fragments, useful in treatment and diagnosis of cancer, rheumatoid
 PT arthritis and coronary heart disease -

PS Claim 30: Page 148; 163pp; English.

CC The present sequence represents the light chain of an antibody reactive
 CC against p53. The antibody is obtained from a vertebrate host expressing
 CC an immune response against a naturally occurring disease. The antibodies
 CC are useful in pharmaceutical compositions, which additionally contain
 CC chelators, drugs, produgs, toxins and imaging markers e.g. radioisotopes
 CC or gadolinium. The polypeptide components of the antibodies are useful in
 CC vaccines, for inducing an immune response against a disease in a
 CC vertebrate, for treatment and/or prophylaxis of disease and for detection
 CC purposes. The nucleic acid sequences can be used to detect a disease as
 CC well as for gene therapy and recombinant production of the polypeptides.
 CC In particular, the following can be treated cancer, rheumatoid arthritis
 CC and coronary heart disease. Cancers include carcinogenic tumours, tumours
 CC of epithelial origin, e.g. colo-rectal cancer, breast cancer lung cancer,
 CC head and neck tumours, hepatic cancer, pancreatic cancer, ovarian cancer,
 CC gastric cancer, brain cancer, bladder cancer, prostate cancer, and
 CC urinary/genital tract cancer, oesophageal cancer, mesenchymal tumours,
 CC e.g. sarcoma, and hemopoietic tumours, e.g. B cell lymphoma.

Sequence 113 AA:

Query Match 43.8%; Score 63; DB 21; Length 113;
 Best Local Similarity 77.8%; Pred. No. 0.29;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGGDTATAPASSLQAD 29
 ||||| | |||||

Mon Jul 15, 13:58:19 2002

us-09-712-819a-10.open.rag

Page 9

db 71 sgsqtdftlrlsalsged 88

Search completed: July 15, 2002, 12:57:59
job time: 415 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2002, 12:59:20 : Search time 75.67 Seconds
(without alignments)
9.361 Million cell updates/sec

Title: US-09-712-819A-10

Perfect score: 144
Sequence: 1 YERKKRRQRSSGTDATAPASSLOAED 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
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5: /cgn2_6/ptodata/2/1aa/PTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/Backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	43.8	80	3	US-08-554-840-13
2	63	43.8	80	3	US-08-554-840-15
3	63	43.8	107	3	US-08-554-840-2
4	63	43.8	107	4	US-08-525-539A-81
5	63	43.8	112	1	US-07-942-245-30
6	63	43.8	113	1	US-08-467-420A-21
7	63	43.8	113	1	US-08-470-110A-21
8	63	43.8	113	1	US-08-667-769A-21
9	63	43.8	113	2	US-08-940-371-21
10	63	43.8	113	3	US-08-637-647-21
11	63	43.8	113	4	US-08-525-539A-80
12	63	43.8	113	5	PCT-US93-08435-6
13	63	43.8	113	5	PCT-US93-08435-8
14	63	43.8	113	5	PCT-US95-17082A-21
15	63	43.8	114	1	US-08-360-125-6
16	63	43.8	114	1	US-08-450-578-6
17	63	43.8	114	2	US-09-017-628-6
18	63	43.8	114	2	US-09-014-880-6
19	63	43.8	114	4	US-09-025-769B-17
20	63	43.8	115	4	US-09-025-769B-31
21	63	43.8	115	4	US-09-025-769B-49
22	63	43.8	127	1	US-08-026-320A-4
23	63	43.8	127	4	US-08-525-539A-65
24	63	43.8	131	2	US-08-483-636-14
25	63	43.8	131	2	US-08-483-636-58
26	63	43.8	131	2	US-08-483-632-14
27	63	43.8	131	2	US-08-483-632-58

28	63	43.8	133	3	US-08-463-903-4	Sequence 4, Appl 1
29	63	43.8	133	4	US-07-935-695-4	Sequence 4, Appl 1
30	63	43.8	155	3	US-08-812-586-46	Sequence 46, Appl 1
31	63	43.8	155	3	US-08-828-741B-11	Sequence 11, Appl 1
32	63	43.8	155	4	US-09-160-567-11	Sequence 11, Appl 1
33	63	43.8	171	3	US-08-463-903-20	Sequence 20, Appl 1
34	63	43.8	171	4	US-07-935-695-20	Sequence 20, Appl 1
35	63	43.8	241	2	US-07-916-098A-56	Sequence 56, Appl 1
36	63	43.8	260	3	US-08-463-903-2	Sequence 2, Appl 1
37	63	43.8	260	4	US-07-935-695-2	Sequence 2, Appl 1
38	63	43.8	275	3	US-08-463-903-6	Sequence 6, Appl 1
39	63	43.8	275	4	US-07-935-695-6	Sequence 6, Appl 1
40	63	43.8	285	3	US-08-463-903-22	Sequence 22, Appl 1
41	63	43.8	285	4	US-07-935-695-22	Sequence 22, Appl 1
42	63	43.8	342	3	US-08-828-741B-6	Sequence 6, Appl 1
43	63	43.8	342	4	US-09-160-567-6	Sequence 6, Appl 1
44	63	43.8	495	3	US-08-828-741B-4	Sequence 4, Appl 1
45	63	43.8	495	4	US-09-160-567-4	Sequence 4, Appl 1

ALIGNMENTS

RESULT 1
US-08-554-840-13
Sequence 13, Application US/08554840
Patent No. 6001358
GENERAL INFORMATION:
APPLICANT: BLACK, Amelia
APPLICANT: HANNA, Nabli
APPLICANT: PADLAN, Eduardo A.
APPLICANT: NEWMAN, Roland A.
TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN gp39,
TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,840
FILING DATE: 07-NOV-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Teekin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-554-840-13
Query Match 43.8%; Score 63; DB 3; Length 80;
Best Local Similarity 77.8%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
By 12 SGSGTDATAPASSLOAED 29

DB 47 SSGSTDFLTITSSLOAED 64

```

RESULT 2
US-08-554-840-15
; Sequence 15, Application US/08554840
; Patent No. 6001358
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN GP39,
; TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,840
; FILING DATE: 07-NOV-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-554-840-15

Query Match 43.8%; Score 63; DB 3; Length 80;
Best Local Similarity 77.8%; Pred. No. 0.03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGSDATAPASSLOAED 29
DB 47 SSGSTDFLTITSSLOAED 64

RESULT 3
US-08-554-840-2
; Sequence 2, Application US/08554840
; Patent No. 6001358
; GENERAL INFORMATION:
; APPLICANT: BLACK, Amelia
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: NEMAN, Roland A.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES TO HUMAN GP39,
; TITLE OF INVENTION: COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,840
; FILING DATE: 07-NOV-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-554-840-2

Query Match 43.8%; Score 63; DB 3; Length 107;
Best Local Similarity 77.8%; Pred. No. 0.041;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGSDATAPASSLOAED 29
DB 65 SSGSTDFLTITSSLOAED 82

RESULT 4
US-08-525-539A-81
; Sequence 81, Application US/0852539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
```

```

; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,840
; FILING DATE: 07-NOV-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-554-840-2
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```

Query Match 43.8%; Score 63; DB 3; Length 107;
Best Local Similarity 77.8%; Pred. No. 0.041;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGSDATAPASSLOAED 29
DB 65 SSGSTDFLTITSSLOAED 82
```

```

RESULT 4
US-08-525-539A-81
; Sequence 81, Application US/0852539A
; Patent No. 6309636
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.R.
; APPLICANT: CERIANI, ROBERTO L.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; TITLE OF INVENTION: MC3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
; TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/525,539A
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DYLAN, TYLER
; REGISTRATION NUMBER: 37,612
; REFERENCE/DOCKET NUMBER: 27633-20001.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
```

TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-525-539A-81

Query Match 43.8%; Score 63; DB 4; Length 107;
Best Local Similarity 77.8%; Pred. No. 0.041;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGCTDATAFASTAQAED 29
||||| |
DB 65 SSGCTDFTLTISSQAED 82

RESULT 5
US-07-942-245-30
Sequence 30, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GULLD, Bryndon C.
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughree, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942.245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-942-245-30

Query Match 43.8%; Score 63; DB 1; Length 112;
Best Local Similarity 77.8%; Pred. No. 0.043;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGCTDATAFASTAQAED 29
||||| |
DB 71 SSGCTDFTLTISSQAED 88

RESULT 6
US-08-467-420A-21

Sequence 21, Application US/08467420A
Patent No. 5683892
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful In
TREATMENT OF SEVERE ALLERGIC REACTIONS
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESS: Intellectual Property
STREET: P. O. Box 1539-0W2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467.420A
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5024
TELEFAX: 610 270-5090
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-420A-21

Query Match 43.8%; Score 63; DB 1; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.043;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGCTDATAFASTAQAED 29
||||| |
DB 71 SSGCTDFTLTISSQAED 88

RESULT 7
US-08-470-110A-21
Sequence 21, Application US/08470110A
Patent No. 5693323
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.

TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
 TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
 NUMBER OF SEQUENCES: 74
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham Corp./Corporate
 ADDRESSEE: Intellectual Property
 STREET: P. O. Box 15139-0W2220
 CITY: King of Prussia
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19406-0939
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/470,110A
 FILING DATE:
 CLASSIFICATION: 426
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/365131
 FILING DATE: 23-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Sutton, Jeffrey A.
 REGISTRATION NUMBER: 34,028
 REFERENCE/DOCKET NUMBER: P50282
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610 270-5024
 TELEFAX: 610 270-5090
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 113 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-470-110A-21

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Query Match: 43.8%; Score 63; DB 1; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.043;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

0Y      12  SCSCTDATAPASSLOAED 29
          |||||+|||||
          |||||+|||||
Db       71  SCSCTDFTLTISLOAED 88

RESULT 8
US-08-667-769A-21
: Sequence 21, Application US/08667769A
: Patent No. 5783184
: GENERAL INFORMATION:
  APPLICANT: Ames, Robert S.
  APPLICANT: Appelbaum, Edward R.
  APPLICANT: Chaiken, Irwin M.
  APPLICANT: Cook, Richard W.
  APPLICANT: Gross, Mitchell S.
  APPLICANT: Holmes, Stephen D.
  APPLICANT: McMillan, Lynette J.
  APPLICANT: Theisen, Timothy W.
  TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
  TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
  NUMBER OF SEQUENCES: 76
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: SmithKline Beecham Corp./Corporate
  STREET: P.O. Box 1539-WR2220
  CITY: King of Prussia
  STATE: Pennsylvania
  COUNTRY: USA
  ZIP: 19406-0939
: COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Systemin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/667,769A
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/17082
 FILING DATE: 22-DEC-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/470110
 FILING DATE: 06-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/467420
 FILING DATE: 06-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/365131
 FILING DATE: 23-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Sutron, Jeffrey A.
 REGISTRATION NUMBER: 34,028
 REFERENCE/DOCKET NUMBER: P50503
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-5024
 TELEFAX: 610-270-5090
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 113 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-667-769A-21

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Query Match: 43.8%; Score 63; DB 1; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.043;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0.

QY      12  SGSGTDATAPASSLQAED 29
      ||||| | |||||
      71  SGSGTDFLTIRISSLQAED 88

Db

RESULT      9
US-08-940-371-21
Sequence 21  Application US/08940371
Patent No. 5851525
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful In
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P. O. Box 1539-0W2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,371
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/470,110
FILING DATE:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5024
TELEFAX: 610 270-5090
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-940-371-21

Query Match 43.8%; Score 63; DB 2; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.043;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGSCTDTPASSLOAED 29
Db 71 SSGSCTDFTLTSSLOAED 88

RESULT 10
US-08-637-647-21
Sequence 21, Application US/08637647
Patent No. 6129613
GENERAL INFORMATION:
APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
APPLICANT: Cook, Richard M.
APPLICANT: Gross, Mitchell S.
APPLICANT: McMillan, Lynette J.
APPLICANT: Theisen, Timothy W.
TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SmithKline Beecham Corp./Corporate
STREET: P. O. Box 1539-UM2220
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,647
FILING DATE: 19-JUN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/363,131
FILING DATE:
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5024
TELEFAX: 610 270-5090
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-637-647-21

Query Match 43.8%; Score 63; DB 3; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.043;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 12 SSGSCTDTPASSLOAED 29
Db 71 SSGSCTDFTLTSSLOAED 88

RESULT 11
US-08-525-539A-80
Sequence 80, Application US/08525539A
Patent No. 6309636
GENERAL INFORMATION:
APPLICANT: DO COUTO, FERNANDO J.R.
APPLICANT: CERIANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
TITLE OF INVENTION: M3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORRISON & ROEMER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 27633-20001.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-525-539A-80

Query Match 43.8%; Score 63; DB 4; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.043;

Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 12 SSGCTDATAASSLOAED 29
|||||||1|||||||
Db 71 SSGCTDFTLTISSLOAED 88

RESULT 12
PCT-US93-08435-6
; Sequence 6, Application PC/TUS9308435
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Navy
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Army
; TITLE OF INVENTION: Novel Antibodies for Conferring Passive
; TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 Norristown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,654
; FILING DATE: 09-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: SRC P50107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9200
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-08435-6

Query Match 43.8%; Score 63; DB 5; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.043;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 12 SSGCTDATAASSLOAED 29
|||||||1|||||||
Db 71 SSGCTDFTLTISSLOAED 88

RESULT 13
PCT-US93-08435-8
; Sequence 8, Application PC/TUS9308435
; GENERAL INFORMATION:
; APPLICANT: SmithKline Beecham, Corporation
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Navy
; APPLICANT: U. S. Government, Secretary of
; APPLICANT: the Army
; TITLE OF INVENTION: Novel Antibodies for Conferring Passive

;; TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
;; NUMBER OF SEQUENCES: 61
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Howson and Howson
;; STREET: Box 457, 321 Norristown Road
;; CITY: Spring House
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19477
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US93/08435
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/941,654
;; FILING DATE: 09-SEP-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bak, Mary E.
;; REGISTRATION NUMBER: 31,215
;; REFERENCE/DOCKET NUMBER: SRC P50107
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 540-9200
;; TELEFAX: (215) 540-5818
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 113 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
PCT-US93-08435-8

Query Match 43.8%; Score 63; DB 5; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.043;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 12 SSGCTDATAASSLOAED 29
|||||||1|||||||
Db 71 SSGCTDFTLTISSLOAED 88

RESULT 14
PCT-US93-17082A-21
; Sequence 21, Application PC/TUS9317082A
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; STREET: P.O. Box 1539-0W2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17082A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470110
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467420
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50282-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-17082A-21

Query Match 43.8%; Score 63; DB 5; Length 113;
Best Local Similarity 77.8%; Pred. No. 0.043;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGSDATAPASSLOAED 29
DB 71 SSGSDFTLTSSLOAED 88

RESULT 15
US-08-360-125-6
Sequence 6, Application US/08360125
Patent No. 5767246
GENERAL INFORMATION:
APPLICANT: Saiko HOSOKAWA
APPLICANT: Toshiaki TAGAWA
APPLICANT: Yoko HIRAKAWA
APPLICANT: No. 5767246hiko ITO
APPLICANT: Kazuhiro NAGAIKE
TITLE OF INVENTION: Human Monoclonal Antibody
SPECIFICALLY Binding to Surface Antigen of Cancer
TITLE OF INVENTION: Cell Membrane
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Menderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360.125
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/905,534
FILING DATE: June 29, 1992
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: Hybridoma producing human
CELL LINE: antibody GAH
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-6

Query Match 43.8%; Score 63; DB 1; Length 114;
Best Local Similarity 77.8%; Pred. No. 0.044;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 SSGSDATAPASSLOAED 29
DB 71 SSGSDFTLTSSLOAED 88

Search completed: July 15, 2002, 12:59:20
Job time: 391 sec

